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(54) **DNA SEQUENCES FROM TCD GENOMIC REGION OF *PHOTORHABDUS LUMINESCENS***

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(51) **Int. Cl.**

A01H 5/00	(2006.01)
A01H 5/10	(2006.01)
C12N 15/82	(2006.01)
C12N 15/31	(2006.01)

(52) **U.S. Cl.** **800/302**; 536/23.7; 435/418

(58) **Field of Classification Search** .... None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,281,413 B1 *	8/2001	Kramer et al.	800/302
2002/0078478 A1	6/2002	Waterfield et al.	

FOREIGN PATENT DOCUMENTS

WO	WO 01/11029 A	2/2001

OTHER PUBLICATIONS

Database EMBL 'Online! , Oct. 27, 2001, XP002290086 retrieved from EBI Database accession No. AF346500 abstract.

Waterfield N. R. et. al.: "The tc genes of *Photorhabdus*: A growing family" Trends in Microbiology, Elsevier Science Ltd., Kidlington, GB, vol. 9, No. 4, Apr. 2001, pp. 181-191 xp002221683.

Ffrench-Constant R H et al: "A genomic sample sequence of the entomopathogenic bacterium *Photorhabdus luminescens* W14: Potential implications for virulence" Applied and Environmental Microbiology, Washington, DC US, vol. 66, No. 8, Aug. 2000, pp. 3310-3329.

Waterfield N. et al: "Oral toxicity of *Photorhabdus luminescens* W14 toxin complexes in *Escherichia coli*" Applied Environmental Microbiology, Washington, DC, US, vol. 67, No. 11, Nov. 2001, pp. 5017-5024.

Ffrench-Constant R et al: "*Photorhabdus* toxins: novel biological insecticides." Current Opinion in Microbiology. Jun. 1999, vol. 2, No. 3, Jun. 1999, pp. 284-328.

Ffrence-Constant R H et al: "Novel insecticidal toxins from nematode-symbiotic bacteria" CMLS Cellular and Molecular Life Sciences, vol. 57, No. 5, May 2000, pp. 828-833.

Waterfield Nicholas R et al: "Genomic islands in *Photorhabdus*." Trends in Microbiology, vol. 10, No. 12, Dec. 2002, pp. 541-545.

* cited by examiner

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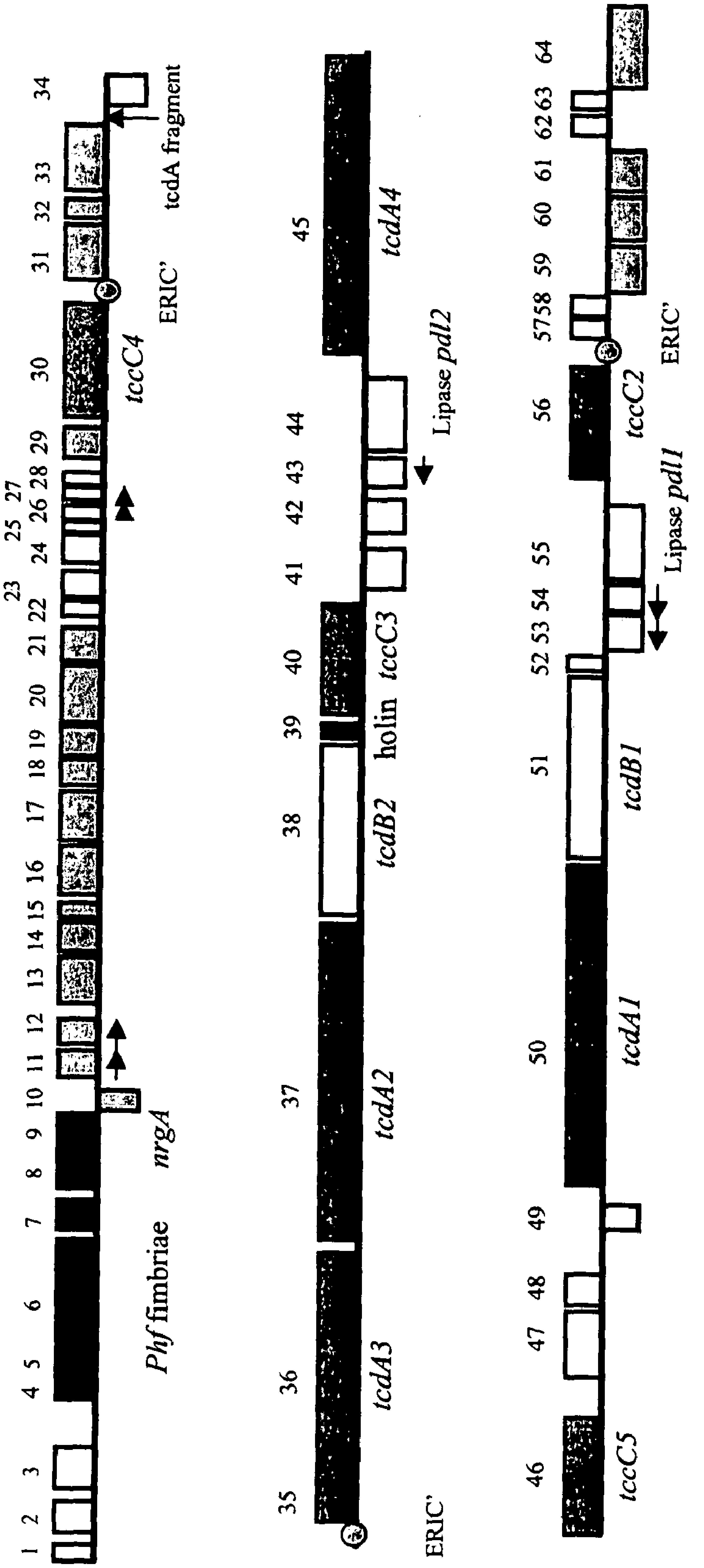
(57) **ABSTRACT**

Nucleotide sequences for seven genes, tccC4, tcdA3, tcdA2, tcdB2, tccC3, tcdA4, tccC5, from the tcd genomic region of *Photorhabdus luminescens* W-14, are useful in heterologous expression of orally active insect toxins.

11 Claims, 1 Drawing Sheet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ERIC'
tcdA fragment
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ERIC'

Fig. 1

DNA SEQUENCES FROM TCD GENOMIC REGION OF *PHOTORHABDUS LUMINESCENS*

This application is a division of U.S. Ser. No. 10/706,424, filed Nov. 12, 2003, now U.S. Pat. No. 7,268,275, which claims the benefit of U.S. Ser. No. 60/425,672, filed Nov. 12, 2002.

This invention provides genes from the tcd genomic region of *Photorhabdus luminescens* (W-14) that are useful in heterologous expression of orally active insect toxins.

BACKGROUND OF THE INVENTION

As reported in WO98/08932, protein toxins from the genus *Photorhabdus* have been shown to have oral toxicity against insects. The toxin complex produced by *Photorhabdus luminescens* (W-14), for example, has been shown to contain ten to fourteen proteins, and it is known that these are produced by expression of genes from four distinct genomic regions: tca, tcb, tcc, and tcd. WO98/08932 discloses nucleotide sequences for many of the native toxin genes, including the toxin gene referred to hereinafter as tcdA1.

Of the separate toxins isolated from *Photorhabdus luminescens* (W-14), those designated Toxin A and Toxin B have been the subject of focused investigation for their activity against target insect species of interest, for example corn rootworm. Toxin A is comprised of two different subunits. The native gene tcdA1 (SEQ ID NO:1) encodes protoxin TcdA (see SEQ ID NO: 1). As determined by mass spectrometry, TcdA1 is processed by one or more proteases to provide Toxin A. More specifically, TcdA1 is an approximately 282.9 kDA protein (2516 aa) that is processed to provide TcdAii, an approximately 208.2 kDA (1849 aa) protein encoded by nucleotides 265-5811 of SEQ ID NO: 1, and TcdAiii, an approximately 63.5 kDA (579 aa) protein encoded by nucleotides 5812-7551 of SEQ ID NO:1.

WO 01/11029 discloses nucleotide sequences that encode TcdA1 and TcbA and have base compositions that have been altered from that of the native genes to make them more similar to plant genes. Also disclosed are transgenic plants that express Toxin A and Toxin B.

Heterologous expression of Toxin A does not afford the level of oral toxicity to insects that is observed for the native toxin. It would be very valuable if means could be found to enhance the level of toxicity of heterologously expressed Toxin A.

Published United States Patent Application 2002/0078478 discloses nucleotide sequences for two genes, tcdB and tccC2, from the tcd genomic region of *Photorhabdus luminescens* (W-14), and discloses that co-expression of tcdB and tccC2 with tcdA1 in heterologous hosts results in enhanced levels of oral insect toxicity compared to that obtained when tcdA1 is expressed alone in such heterologous hosts. The tcdB gene disclosed in Published United States Patent Application 2002/0078478 is referred to hereinafter as tcdB1.

SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences for seven newly discovered genes, tccC4, tcdA3, tcdA2, tcdB2, tccC3, tcdA4, tccC5, from the tcd genomic region of *Photorhabdus luminescens* W-14. The genes can be used to express orally active insect toxins in heterologous hosts.

Three of these genes, tccC3, tccC4, tccC5, can be used in the same way that tccC2 is used, and one of them, tcdB2 can be used in the same way that tcdB1 is used, as disclosed in Published United States Patent Application 2002/0078478, hereby incorporated by reference, to obtain enhanced levels of oral insect activity when co-expressed with tcdA1. The tcdA3, tcdA2, and tcdA4 genes are similar to tcdA1 and are therefore expected to have similar utility as insect toxin genes.

In one embodiment of the invention tcdA1 and tcdB1 are expressed with a gene selected from tccC3, tccC4, or tccC5 in a host other than *Photorhabdus luminescens* W-14, for example in a plant.

In a second embodiment of the invention tcdA1 and tcdB2 are expressed with a gene selected from tccC2, tccC3, tccC4, or tccC5 in a host other than *Photorhabdus luminescens* W-14, for example in a plant.

BRIEF DESCRIPTION OF THE FIGURE

FIG. **1** illustrates a portion of the toxin complex d (tcd) island from *Photorahbdus luminescens.*

SUMMARY OF THE SEQUENCES

SEQ ID NO: 1 is the DNA sequence for tcdA1 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 2 is the amino acid sequence for TcdA1 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 3 is the DNA sequence for tcdA2 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 4 is the amino acid sequence for TcdA2 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 5 is the DNA sequence for tcdA3 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 6 is the amino acid sequence for TcdA3 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 7 is the DNA sequence for tcdA4 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 8 is the amino acid sequence for TcdA4 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 9 is the DNA sequence for tcdB2 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 10 is the amino acid sequence for TcdB2 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 11 is the DNA sequence for tccC3 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 12 is the amino acid sequence for TccC3 from from *Photorhabdus luminescens* W-14.

SEQ ID NO: 13 is the DNA sequence for tccC4 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 14 is the amino acid sequence for TccC4 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 15 is the DNA sequence for tccC5 from *Photorhabdus luminescens* W-14.

SEQ ID NO: 16 is the amino acid sequence for TccC5 from *Photorhabdus luminescens* W-14.

DETAILED DESCRIPTION OF THE INVENTION

To isolate islands unique to *Photorhabdus* we end-sequenced an arrayed cosmid library of the W-14 strain and compared the end-sequences with those in public databases using BLAST algorithms. Unique cosmids were sequenced and checked for pathogenic phenotypes, such as the ability to persist within, or kill, insects. As all *Photorhabdus* strains (even clinical isolates) are pathogenic to insects, we identified genomic islands by gene homology (BlastX), relative location in the genome (tRNA linkage or within *E. coli*-like core sequence) or altered GC content (estimated as 41.5% for the W14 core).

FIG. **1** illustrates a portion of the toxin complex d (tcd) island from *P. luminescens* W14 (accession AY144119). This unique island carries multiple copies of toxin complex (tc) genes. The tc genes encode high molecular weight insecticidal Toxin complexes or Tc's which destroy the insect midgut. The island carries multiple tcdA-like genes (ORFs 36, 37, 45 and 50) and tcdB-like genes like genes(ORFs 38 and 51). The region also carries multiple tccC-like genes (ORFs 30, 40, 46 and 56), ERIC-like (Enteric Repetitive Intergenic Consensus) sequences (see Versalovic, J. et al. (1991) Distribution of repetitive DNA sequences in eubacteria and application to fingerprinting of bacterial genomes. *Nucleic Acids Res* 19 (24), 6823-6831.), duplicated ORFs (luxR-like regulators), and a truncated tcdA-like gene.

It is preferred for the nucleic acids according to the invention to comprise at least one sequence chosen from

(a) the sequences according to SEQ ID NOS: 3, 5, 7, 9, 11, 13, and 15.
(b) at least 14 base pairs-long partial sequences of the sequences defined under (a),
(c) sequences that hybridize with the sequences defined under (a),
(d) sequences that are at least 70%, preferably 80% and even more preferred, 90% identical to the sequences defined under (a),
(e) sequences that are at least 70%, preferably 80% and even more preferred, 90% similar to the sequences defined under (a),
(f) sequences that complement the sequences defined under (a), and
(g) sequences that due to the degeneracy of the genetic code, code for the same amino acid sequence as(i.e. are "isocoding" with) the sequences defined under (a) through (e).

The expression "hybridize" as used herein refers to hybridization under the following specified conditions: 5×SSC; blocking reagent (Roche Diagnostics Inc., Mannheim, Germany), 1%; N-lauroyl-sarcosine, 0.1%; SDS (sodium-dodecyl sulfate) 0.02%; hybridization temperature: 60° C.; first wash step: 2×SSC at 60° C.; second wash step: 2×SSC at 60° C.; preferred second wash step: 0.5×SSC at 60° C.; especially preferred second wash step: 0.2×SSC at 60° C.

"Identity" and "similarity" are scored by the GAP algorithm using the Blosum 62 protein scoring matrix (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, Wis.).

Expression of the Nucleotide Sequences in Heterolopous Microbial Hosts

As biological insect control agents, the insecticidal toxins are produced by expression of the nucleotide sequences in heterologous host cells capable of expressing the nucleotide sequences. In a first embodiment, additional copies of one or more of the nucleotide sequences are added to *Xenorhabdus nematophilus, Xenorhabdus poinarii*, or *Photorhabdus luminescens* cells either by insertion into the chromosome or by introduction of extrachromosomally replicating molecules containing the nucleotide sequences.

In another embodiment, at least one of the nucleotide sequences of the invention is inserted into an appropriate expression cassette, comprising a promoter and termination signals. Expression of the nucleotide sequence is constitutive, or an inducible promoter responding to various types of stimuli to initiate transcription is used. In a preferred embodiment, the cell in which the toxin is expressed is a microorganism, such as a virus, a bacteria, or a fungus. In a preferred embodiment, a virus, such as a baculovirus, contains a nucleotide sequence of the invention in its genome and expresses large amounts of the corresponding insecticidal toxin after infection of appropriate eukaryotic cells that are suitable for virus replication and expression of the nucleotide sequence. The insecticidal toxin thus produced is used as an insecticidal agent. Alternatively, baculoviruses engineered to include the nucleotide sequence are used to infect insects in-vivo and kill them either by expression of the insecticidal toxin or by a combination of viral infection and expression of the insecticidal toxin.

Bacterial cells are also hosts for the expression of the nucleotide sequences of the invention. In a preferred embodiment, non-pathogenic symbiotic bacteria, which are able to live and replicate within plant tissues, so-called endophytes, or non-pathogenic symbiotic bacteria, which are capable of colonizing the *phyllosphere* or the *rhizosphere*, so-called epiphytes, are used. Such bacteria include bacteria of the genera *Agrobacterium, Alcaligenes, Azospiriilum, Azotobacter, Bacillus, Ciavibacter, Enterobacter, Erwinia, Flavobacter, Klebsielia, Pseudomonas, Rhizobium, Serratia, Streptomyces* and *Xanthomonas*. Symbiotic fungi, such as Trichoderma and Gliocladium are also possible hosts for expression of the inventive nucleotide sequences for the same purpose.

Techniques for these genetic manipulations are specific for the different available hosts and are known in the art. For example, the expression vectors pKK223-3 and pKK223-2 can be used to express heterologous genes in *E. coli*, either in transcriptional or translational fusion, behind the tac or trc promoter. For the expression of operons encoding multiple ORFS, the simplest procedure is to insert the operon into a vector such as pKK2233 in transcriptional fusion, allowing the cognate ribosome binding site of the heterologous genes to be used. Techniques for overexpression in gram-positive species such as *Bacillus* are also known in the art and can be used in the context of this invention (Quax et al. In.: Industrial Microorganisms: Basic and Applied Molecular Genetics, Eds. Baltz et al., American Society for Microbiology, Washington (1993)). Alternate systems for overexpression rely for example, on yeast vectors and include the use of *Pichia, Saccharomyces* and *Kluyveromyces* (Sreekrishna, In: industrial microorganisms: basic and applied molecular genetics, Baltz, Hegeman, and Skatrud eds., American Society for Microbiology, Washington (1993); Dequin & Barre, Biotechnology 12:173-177 (1994); van den Berg et al., Biotechnology 8:135-139 (1990)).

Expression of the Nucleotide Sequences in Plant Tissue

In a particularly preferred embodiment, at least one of the insecticidal toxins of the invention is expressed in a higher organism, e.g., a plant. In this case, transgenic plants expressing effective amounts of the toxins protect themselves from insect pests. When the insect starts feeding on such a transgenic plant, it also ingests the expressed toxins. This will deter the insect from further biting into the plant tissue or may even harm or kill the insect. A nucleotide sequence of the present invention is inserted into an expression cassette, which is then preferably stably integrated in the genome of said plant, In another preferred embodiment, the nucleotide sequence is included in a non-pathogenic self-replicating virus. Plants transformed in accordance with the present invention may be monocots or dicots and include, but are not limited to, maize, wheat, barley, rye, sweet potato, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, pepper, celery, squash, pumpkin, hemp, zucchini, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tomato, sorghum, sugarcane, sugarbeet, sunflower, rapeseed, clover, tobacco, carrot, cotton, alfalfa, rice, potato, eggplant, cucumber, Arabidopsis, and woody plants such as coniferous and deciduous trees.

Once a desired nucleotide sequence has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques.

A nucleotide sequence of this invention is preferably expressed in transgenic plants, thus causing the biosynthesis of the corresponding toxin in the transgenic plants. In this way, transgenic plants with enhanced resistance to insects are generated. For their expression in transgenic plants, the nucleotide sequences of the invention may require modification and optimization. Although in many cases genes from microbial organisms can be expressed in plants at high levels without modification, low expression in transgenic plants may result from microbial nucleotide sequences having codons that are not preferred in plants. It is known in the art that all organisms have specific preferences for codon usage, and the codons of the nucleotide sequences described in this invention can be changed to conform with plant preferences, while maintaining the amino acids encoded thereby. Furthermore, high expression in plants is best achieved from coding sequences that have at least about 35% GC content, preferably more than about 45%, more preferably more than about 50%, and most preferably more than about 60%. Microbial nucleotide sequences which have low GC contents may express poorly in plants due to the existence of ATTTA motifs which may destabilize messages, and AATAAA motifs which may cause inappropriate polyadenylation. Although preferred gene sequences may be adequately expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray et al. Nucl. Acids Res. 17:477-498 (1989)). In addition, the nucleotide sequences are screened for the existence of illegitimate splice sites that may cause message truncation. All changes required to be made within the nucleotide sequences such as those described above are made using well known techniques of site directed mutagenesis, PCR, and synthetic gene construction.

For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be effective in plants. Joshi has suggested an appropriate consensus for plants (NAR 15:6643-6653 (1987)) and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensuses are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. Thus, expression of the nucleotide sequences of this invention in leaves, in ears, in inflorescences (e.g. spikes, panicles, cobs, etc.), in roots, and/or seedlings is preferred. In many cases, however, protection against more than one type of insect pest is sought, and thus expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and vice versa, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CAMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the insecticidal toxins to be synthesized only when the crop plants are treated with the inducing chemicals.

A preferred category of promoters is that which is wound inducible. Numerous promoters have been described which are expressed at wound sites and also at the sites of phytopathogen infection. Ideally, such a promoter should only be active locally at the sites of infection, and in this way the insecticidal toxins only accumulate in cells which need to synthesize the insecticidal toxins to kill the invading insect pest. Preferred promoters of this kind include those described by Stanford et al. Mol. Gen. Genet. 215:200-208 (1989), Xu et al. Plant Molec. Biol. 22:573-588 (1993), Logemann et al. *Plant Cell* 1:151-158 (1989), Rohrmieier & Lehle, Plant Molec. Biol. 22:783-792 (1993), Firek et al. Plant Molec. Biol. 22:129-142 (1993), and Warner et al. Plant J. 3:191-201 (1993).

Especially preferred embodiments of the invention are transgenic plants expressing at least one of the nucleotide sequences of the invention in a root-preferred or root-specific fashion. Further preferred embodiments are transgenic plants expressing the nucleotide sequences in a wound-inducible or pathogen infection-inducible manner.

In addition to the selection of a suitable promoter, constructions for expression of an insecticidal toxin in plants require an appropriate transcription terminator to be attached downstream of the heterologous nucleotide sequence. Several such terminators are available and known in the art (e.g. tml from *Agrobacterium*, E9 from rbcs). Any available terminator known to function in plants can be used in the context of this invention.

Numerous other sequences can be incorporated into expression cassettes described in this invention. These include sequences which have been shown to enhance expression such as intron sequences (e.g. from Adhl and bronzel) and viral leader sequences (e.g. from TMV, MCMV and AMV).

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle may be preferred. Subcellular localization of transgene encoded enzymes is undertaken using techniques well known in the art Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

Vectors suitable for plant transformation are described elsewhere in this specification. For Agrobacterium-mediated transformation, binary vectors or vectors carrying at least one

T-DNA border sequence are suitable, whereas for direct gene transfer any vector is suitable and linear DNA containing only the construction of interest may be preferred. In the case of direct gene transfer, transformation with a single DNA species or co-transformation can be used (Schocher et al. Biotechnology 4: 1093-1096 (1986)). For both direct gene transfer and Agrobacterium-mediated transfer, transformation is usually (but not necessarily) undertaken with a selectable or screenable marker which may provide resistance to an antibiotic (kanamycin, hygromycin or methotrexate) or a herbicide (Basta). Examples of such markers are neomycin phosphotransferase, hygromycin phosphotransferase, dihydrofolate reductase, phosphinothricin acetyltransferase, 2,2-dichloroproprionic acid dehalogenase, acetohydroxyacid synthase, 5-enolpyruvyl-shikimate-phosphate synthase, haloarylnitrilase, protoporhyrinogen oxidase, acetyl-coenzyme A carboxylase, dihydropteroate synthase, chloramphenicol acetyl transferase, and β-glucuronidase. The choice of selectable or screenable marker for plant transformation is not, however, critical to the invention.

The recombinant DNA described above can be introduced into the plant cell in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of plant targeted for transformation. Suitable methods of transforming plant cells include microinjection (Crossway et al., BioTechniques 4.,320-334 (1 986)), electroporation (Riggs et al., Proc. Natl. Acad, Sci. USA 83.,5602-5606 (1986), Agrobacterium-mediated transformation (Hinchee et al., Biotechnology 6:915-921 (**1988**); See also, Ishida et al., Nature Biotechnology 14:745-750 (June 1996) (for maize transformation), direct gene transfer (Paszkowski et al., EMBO J. 3.2717-2722 (1984); Hayashimoto et al., Plant Physiol 93.857-863 (1990)(rice), and ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wis. and Dupont, Inc., Wilmington, Del. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., Biotechnology 6.923-926 (1988)). See also, Weissinger et al., Annual Rev Genet. 22.-421-477 (1988); Sanford et al., Particulate Science and Technology 5.27-37 (1987)(onion); Svab et al., Proc. Natl. Acad. Sci. USA 87.-8526-8530 (1990) (tobacco chloroplast); Christou et al., Plant Physiol 87,671-674 (1988)(soybean); McCabe et al., BioTechnology 6.923-926 (1988)(soybean); Klein et al., Proc. Natl. Acad. Sci. USA, 85:4305-4309 (1988) (maize); Klein et al., BioTechnology 6.,559-563 (1988) (maize); Klein et al., Plant PhysioL 91.,440-444 (1988) (maize); Fromm et al., BioTechnology 8:833-839 (1 990); and Gordon-Kamm et al., Plant Cell 2:603-618 (1990) (maize); Koziel et al., Biotechnology 1 1:194-200 (1993) (maize); Shimamoto et al., Nature 338:274-277 (1989) (rice); Christou et al., Biotechnology 9:957-962 (1991) (rice); Datta et al., BioTechnology 8.736-740 (1990) (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., Biotechnology 1 1:1553-1558 (1993) (wheat); Weeks et al., Plant Physiol. 102:1077-1084 (1993) (wheat); Wan et al., Plant Physiol. 104:37-48 (1994) (barley); Jahne et al., Theor. Appl. Genet. 89:525-533 (1994)(barley); Umbeck et al., BioTechnology 5:263-266 (1987) (cotton); Casas et al., Proc. Natl. Acad. Sci. USA 90:11212-11216 (December 1993) (sorghum); Somers et al., BioTechnology 10: 1 589-1594 (December 1992) (oat); Torbert et al., Plant Cell Reports 14:635-640 (1995) (oat); Weeks et al., Plant Physiol. 102:1077-1084 (1993) (wheat); Chang et al., WO 94/13822 (wheat) and Nehra et al., The Plant Journal 5:285-297 (1994) (wheat). A particularly preferred set of embodiments for the introduction of recombinant DNA molecules into maize by microprojectile bombardment can be found in Koziel et al., Biotechnology 11:194-200(1993), Hill et al., Euphytica 85:119-123 (1995) and Koziel et al., Annals of the New York Academy of Sciences 792:164-171 (1996). An additional preferred embodiment is the protoplast transformation method for maize as disclosed in EP 0 292 435. Transformation of plants can be undertaken with a single DNA species or multiple DNA species (i.e. co-transformation).

In another preferred embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. A major advantage of plastid transformation is that plastids are generally capable of expressing bacterial genes without substantial modification, and plastids are capable of expressing multiple open reading frames under control of a single promoter. Plastid transformation technology is extensively described in U.S. Pat. Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al. (1994) Proc. Natl. Acad. Sci. USA 91, 7301-7305. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate homologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab, Z., Hajdukiewicz, P., and Maliga, P. (1990) Proc. Nati. Acad. Sci. USA 87, 8526-8530; Staub, J. M., and Maliga, P. (1992) Plant Cell 4, 39-45). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub, J. M., and Maliga, P. (1993) EMBO J. 12, 601-606). Substantial increases in transformation frequency are obtained by replacement of the recessive RRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial aada gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3' adenyltransferase (Svab, Z., and Maliga, P. (1993) Proc. Natl. Acad. Sci. USA 90, 913-917). Previously, this marker had been used successfully for high-frequency transformation of the plastid genome of the green alga *Chiamydomonas reinhardtii* (Goldschmidt-Clermont, M. (1991) Nucl. Acids Res. 19: 4083-4089). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid expression, in which genes are inserted by homologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

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                              SEQUENCE LISTING


<160> NUMBER OF SEQ ID NOS: 16

<210> SEQ ID NO 1
<211> LENGTH: 7551
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(7548)

<400> SEQUENCE: 1

atg aac gag tct gta aaa gag ata cct gat gta tta aaa agc cag tgt       48
Met Asn Glu Ser Val Lys Glu Ile Pro Asp Val Leu Lys Ser Gln Cys
1               5                   10                  15

ggt ttt aat tgt ctg aca gat att agc cac agc tct ttt aat gaa ttt       96
Gly Phe Asn Cys Leu Thr Asp Ile Ser His Ser Ser Phe Asn Glu Phe
            20                  25                  30

cgc cag caa gta tct gag cac ctc tcc tgg tcc gaa aca cac gac tta      144
Arg Gln Gln Val Ser Glu His Leu Ser Trp Ser Glu Thr His Asp Leu
        35                  40                  45

tat cat gat gca caa cag gca caa aag gat aat cgc ctg tat gaa gcg      192
Tyr His Asp Ala Gln Gln Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala
    50                  55                  60

cgt att ctc aaa cgc gcc aat ccc caa tta caa aat gcg gtg cat ctt      240
Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65                  70                  75                  80

gcc att ctc gct ccc aat gct gaa ctg ata ggc tat aac aat caa ttt      288
Ala Ile Leu Ala Pro Asn Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe
                85                  90                  95

agc ggt aga gcc agt caa tat gtt gcg ccg ggt acc gtt tct tcc atg      336
Ser Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Thr Val Ser Ser Met
            100                 105                 110

ttc tcc ccc gcc gct tat ttg act gaa ctt tat cgt gaa gca cgc aat      384
Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
        115                 120                 125

tta cac gca agt gac tcc gtt tat tat ctg gat acc cgc cgc cca gat      432
Leu His Ala Ser Asp Ser Val Tyr Tyr Leu Asp Thr Arg Arg Pro Asp
    130                 135                 140

ctc aaa tca atg gcg ctc agt cag caa aat atg gat ata gaa tta tcc      480
Leu Lys Ser Met Ala Leu Ser Gln Gln Asn Met Asp Ile Glu Leu Ser
145                 150                 155                 160

aca ctc tct ttg tcc aat gag ctg tta ttg gaa agc att aaa act gaa      528
Thr Leu Ser Leu Ser Asn Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu
                165                 170                 175

tct aaa ctg gaa aac tat act aaa gtg atg gaa atg ctc tcc act ttc      576
Ser Lys Leu Glu Asn Tyr Thr Lys Val Met Glu Met Leu Ser Thr Phe
            180                 185                 190

cgt cct tcc ggc gca acg cct tat cat gat gct tat gaa aat gtg cgt      624
Arg Pro Ser Gly Ala Thr Pro Tyr His Asp Ala Tyr Glu Asn Val Arg
        195                 200                 205

gaa gtt atc cag cta caa gat cct gga ctt gag caa ctc aat gca tca      672
Glu Val Ile Gln Leu Gln Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser
    210                 215                 220

ccg gca att gcc ggg ttg atg cat caa gcc tcc cta ttg ggt att aac      720
Pro Ala Ile Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile Asn
225                 230                 235                 240

gct tca atc tcg cct gag cta ttt aat att ctg acg gag gag att acc      768
Ala Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr
                245                 250                 255
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gaa ggt aat gct gag gaa ctt tat aag aaa aat ttt ggt aat atc gaa      816
Glu Gly Asn Ala Glu Glu Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu
            260                 265                 270

ccg gcc tca ttg gct atg ccg gaa tac ctt aaa cgt tat tat aat tta      864
Pro Ala Ser Leu Ala Met Pro Glu Tyr Leu Lys Arg Tyr Tyr Asn Leu
        275                 280                 285

agc gat gaa gaa ctt agt cag ttt att ggt aaa gcc agc aat ttt ggt      912
Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly
    290                 295                 300

caa cag gaa tat agt aat aac caa ctt att act ccg gta gtc aac agc      960
Gln Gln Glu Tyr Ser Asn Asn Gln Leu Ile Thr Pro Val Val Asn Ser
305                 310                 315                 320

agt gat ggc acg gtt aag gta tat cgg atc acc cgc gaa tat aca acc     1008
Ser Asp Gly Thr Val Lys Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr
                325                 330                 335

aat gct tat caa atg gat gtg gag cta ttt ccc ttc ggt ggt gag aat     1056
Asn Ala Tyr Gln Met Asp Val Glu Leu Phe Pro Phe Gly Gly Glu Asn
            340                 345                 350

tat cgg tta gat tat aaa ttc aaa aat ttt tat aat gcc tct tat tta     1104
Tyr Arg Leu Asp Tyr Lys Phe Lys Asn Phe Tyr Asn Ala Ser Tyr Leu
        355                 360                 365

tcc atc aag tta aat gat aaa aga gaa ctt gtt cga act gaa ggc gct     1152
Ser Ile Lys Leu Asn Asp Lys Arg Glu Leu Val Arg Thr Glu Gly Ala
    370                 375                 380

cct caa gtc aat ata gaa tac tcc gca aat atc aca tta aat acc gct     1200
Pro Gln Val Asn Ile Glu Tyr Ser Ala Asn Ile Thr Leu Asn Thr Ala
385                 390                 395                 400

gat atc agt caa cct ttt gaa att ggc ctg aca cga gta ctt cct tcc     1248
Asp Ile Ser Gln Pro Phe Glu Ile Gly Leu Thr Arg Val Leu Pro Ser
                405                 410                 415

ggt tct tgg gca tat gcc gcc gca aaa ttt acc gtt gaa gag tat aac     1296
Gly Ser Trp Ala Tyr Ala Ala Ala Lys Phe Thr Val Glu Glu Tyr Asn
            420                 425                 430

caa tac tct ttt ctg cta aaa ctt aac aag gct att cgt cta tca cgt     1344
Gln Tyr Ser Phe Leu Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg
        435                 440                 445

gcg aca gaa ttg tca ccc acg att ctg gaa ggc att gtg cgc agt gtt     1392
Ala Thr Glu Leu Ser Pro Thr Ile Leu Glu Gly Ile Val Arg Ser Val
    450                 455                 460

aat cta caa ctg gat atc aac aca gac gta tta ggt aaa gtt ttt ctg     1440
Asn Leu Gln Leu Asp Ile Asn Thr Asp Val Leu Gly Lys Val Phe Leu
465                 470                 475                 480

act aaa tat tat atg cag cgt tat gct att cat gct gaa act gcc ctg     1488
Thr Lys Tyr Tyr Met Gln Arg Tyr Ala Ile His Ala Glu Thr Ala Leu
                485                 490                 495

ata cta tgc aac gcg cct att tca caa cgt tca tat gat aat caa cct     1536
Ile Leu Cys Asn Ala Pro Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro
            500                 505                 510

agc caa ttt gat cgc ctg ttt aat acg cca tta ctg aac gga caa tat     1584
Ser Gln Phe Asp Arg Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr
        515                 520                 525

ttt tct acc ggc gat gag gag att gat tta aat tca ggt agc acc ggc     1632
Phe Ser Thr Gly Asp Glu Glu Ile Asp Leu Asn Ser Gly Ser Thr Gly
    530                 535                 540

gat tgg cga aaa acc ata ctt aag cgt gca ttt aat att gat gat gtc     1680
Asp Trp Arg Lys Thr Ile Leu Lys Arg Ala Phe Asn Ile Asp Asp Val
545                 550                 555                 560

tcg ctc ttc cgc ctg ctt aaa att acc gac cat gat aat aaa gat gga     1728
Ser Leu Phe Arg Leu Leu Lys Ile Thr Asp His Asp Asn Lys Asp Gly
                565                 570                 575
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aaa att aaa aat aac cta aag aat ctt tcc aat tta tat att gga aaa     1776
Lys Ile Lys Asn Asn Leu Lys Asn Leu Ser Asn Leu Tyr Ile Gly Lys
            580                 585                 590

tta ctg gca gat att cat caa tta acc att gat gaa ctg gat tta tta     1824
Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu
        595                 600                 605

ctg att gcc gta ggt gaa gga aaa act aat tta tcc gct atc agt gat     1872
Leu Ile Ala Val Gly Glu Gly Lys Thr Asn Leu Ser Ala Ile Ser Asp
    610                 615                 620

aag caa ttg gct acc ctg atc aga aaa ctc aat act att acc agc tgg     1920
Lys Gln Leu Ala Thr Leu Ile Arg Lys Leu Asn Thr Ile Thr Ser Trp
625                 630                 635                 640

cta cat aca cag aag tgg agt gta ttc cag cta ttt atc atg acc tcc     1968
Leu His Thr Gln Lys Trp Ser Val Phe Gln Leu Phe Ile Met Thr Ser
                645                 650                 655

acc agc tat aac aaa acg cta acg cct gaa att aag aat ttg ctg gat     2016
Thr Ser Tyr Asn Lys Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp
            660                 665                 670

acc gtc tac cac ggt tta caa ggt ttt gat aaa gac aaa gca gat ttg     2064
Thr Val Tyr His Gly Leu Gln Gly Phe Asp Lys Asp Lys Ala Asp Leu
        675                 680                 685

cta cat gtc atg gcg ccc tat att gcg gcc acc ttg caa tta tca tcg     2112
Leu His Val Met Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser
    690                 695                 700

gaa aat gtc gcc cac tcg gta ctc ctt tgg gca gat aag tta cag ccc     2160
Glu Asn Val Ala His Ser Val Leu Leu Trp Ala Asp Lys Leu Gln Pro
705                 710                 715                 720

ggc gac ggc gca atg aca gca gaa aaa ttc tgg gac tgg ttg aat act     2208
Gly Asp Gly Ala Met Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr
                725                 730                 735

aag tat acg ccg ggt tca tcg gaa gcc gta gaa acg cag gaa cat atc     2256
Lys Tyr Thr Pro Gly Ser Ser Glu Ala Val Glu Thr Gln Glu His Ile
            740                 745                 750

gtt cag tat tgt cag gct ctg gca caa ttg gaa atg gtt tac cat tcc     2304
Val Gln Tyr Cys Gln Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser
        755                 760                 765

acc ggc atc aac gaa aac gcc ttc cgt cta ttt gtg aca aaa cca gag     2352
Thr Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu
    770                 775                 780

atg ttt ggc gct gca act gga gca gcg ccc gcg cat gat gcc ctt tca     2400
Met Phe Gly Ala Ala Thr Gly Ala Ala Pro Ala His Asp Ala Leu Ser
785                 790                 795                 800

ctg att atg ctg aca cgt ttt gcg gat tgg gtg aac gca cta ggc gaa     2448
Leu Ile Met Leu Thr Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu
                805                 810                 815

aaa gcg tcc tcg gtg cta gcg gca ttt gaa gct aac tcg tta acg gca     2496
Lys Ala Ser Ser Val Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala
            820                 825                 830

gaa caa ctg gct gat gcc atg aat ctt gat gct aat ttg ctg ttg caa     2544
Glu Gln Leu Ala Asp Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln
        835                 840                 845

gcc agt att caa gca caa aat cat caa cat ctt ccc cca gta act cca     2592
Ala Ser Ile Gln Ala Gln Asn His Gln His Leu Pro Pro Val Thr Pro
    850                 855                 860

gaa aat gcg ttc tcc tgt tgg aca tct atc aat act atc ctg caa tgg     2640
Glu Asn Ala Phe Ser Cys Trp Thr Ser Ile Asn Thr Ile Leu Gln Trp
865                 870                 875                 880

gtt aat gtc gca caa caa ttg aat gtc gcc cca cag ggc gtt tcc gct     2688
Val Asn Val Ala Gln Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala
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                885                 890                 895

ttg gtc ggg ctg gat tat att caa tca atg aaa gag aca ccg acc tat      2736
Leu Val Gly Leu Asp Tyr Ile Gln Ser Met Lys Glu Thr Pro Thr Tyr
            900                 905                 910

gcc cag tgg gaa aac gcg gca ggc gta tta acc gcc ggg ttg aat tca      2784
Ala Gln Trp Glu Asn Ala Ala Gly Val Leu Thr Ala Gly Leu Asn Ser
        915                 920                 925

caa cag gct aat aca tta cac gct ttt ctg gat gaa tct cgc agt gcc      2832
Gln Gln Ala Asn Thr Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala
    930                 935                 940

gca tta agc acc tac tat atc cgt caa gtc gcc aag gca gcg gcg gct      2880
Ala Leu Ser Thr Tyr Tyr Ile Arg Gln Val Ala Lys Ala Ala Ala Ala
945                 950                 955                 960

att aaa agc cgt gat gac ttg tat caa tac tta ctg att gat aat cag      2928
Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln
                965                 970                 975

gtt tct gcg gca ata aaa acc acc cgg atc gcc gaa gcc att gcc agt      2976
Val Ser Ala Ala Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser
            980                 985                 990

att caa ctg tac gtc aac cgg gca  ttg gaa aat gtg gaa  gaa aat gcc   3024
Ile Gln Leu Tyr Val Asn Arg Ala  Leu Glu Asn Val Glu  Glu Asn Ala
        995                 1000                1005

aat tcg  ggg gtt atc agc cgc  caa ttc ttt atc gac  tgg gac aaa      3069
Asn Ser  Gly Val Ile Ser Arg  Gln Phe Phe Ile Asp  Trp Asp Lys
    1010                1015                1020

tac aat  aaa cgc tac agc act  tgg gcg ggt gtt tct  caa tta gtt      3114
Tyr Asn  Lys Arg Tyr Ser Thr  Trp Ala Gly Val Ser  Gln Leu Val
    1025                1030                1035

tac tac  ccg gaa aac tat att  gat ccg acc atg cgt  atc gga caa      3159
Tyr Tyr  Pro Glu Asn Tyr Ile  Asp Pro Thr Met Arg  Ile Gly Gln
    1040                1045                1050

acc aaa  atg atg gac gca tta  ctg caa tcc gtc agc  caa agc caa      3204
Thr Lys  Met Met Asp Ala Leu  Leu Gln Ser Val Ser  Gln Ser Gln
    1055                1060                1065

tta aac  gcc gat acc gtc gaa  gat gcc ttt atg tct  tat ctg aca      3249
Leu Asn  Ala Asp Thr Val Glu  Asp Ala Phe Met Ser  Tyr Leu Thr
    1070                1075                1080

tcg ttt  gaa caa gtg gct aat  ctt aaa gtt att agc  gca tat cac      3294
Ser Phe  Glu Gln Val Ala Asn  Leu Lys Val Ile Ser  Ala Tyr His
    1085                1090                1095

gat aat  att aat aac gat caa  ggg ctg acc tat ttt  atc gga ctc      3339
Asp Asn  Ile Asn Asn Asp Gln  Gly Leu Thr Tyr Phe  Ile Gly Leu
    1100                1105                1110

agt gaa  act gat gcc ggt gaa  tat tat tgg cgc agt  gtc gat cac      3384
Ser Glu  Thr Asp Ala Gly Glu  Tyr Tyr Trp Arg Ser  Val Asp His
    1115                1120                1125

agt aaa  ttc aac gac ggt aaa  ttc gcg gct aat gcc  tgg agt gaa      3429
Ser Lys  Phe Asn Asp Gly Lys  Phe Ala Ala Asn Ala  Trp Ser Glu
    1130                1135                1140

tgg cat  aaa att gat tgt cca  att aac cct tat aaa  agc act atc      3474
Trp His  Lys Ile Asp Cys Pro  Ile Asn Pro Tyr Lys  Ser Thr Ile
    1145                1150                1155

cgt cca  gtg ata tat aaa tcc  cgc ctg tat ctg ctc  tgg ttg gaa      3519
Arg Pro  Val Ile Tyr Lys Ser  Arg Leu Tyr Leu Leu  Trp Leu Glu
    1160                1165                1170

caa aag  gag atc acc aaa cag  aca gga aat agt aaa  gat ggc tat      3564
Gln Lys  Glu Ile Thr Lys Gln  Thr Gly Asn Ser Lys  Asp Gly Tyr
    1175                1180                1185

caa act  gaa acg gat tat cgt  tat gaa cta aaa ttg  gcg cat atc      3609
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Gln Thr  Glu Thr Asp Tyr Arg  Tyr Glu Leu Lys Leu  Ala His Ile
    1190                 1195                 1200

cgc tat  gat ggc act tgg aat  acg cca atc acc ttt  gat gtc aat      3654
Arg Tyr  Asp Gly Thr Trp Asn  Thr Pro Ile Thr Phe  Asp Val Asn
    1205                 1210                 1215

aaa aaa  ata tcc gag cta aaa  ctg gaa aaa aat aga  gcg ccc gga      3699
Lys Lys  Ile Ser Glu Leu Lys  Leu Glu Lys Asn Arg  Ala Pro Gly
    1220                 1225                 1230

ctc tat  tgt gcc ggt tat caa  ggt gaa gat acg ttg  ctg gtg atg      3744
Leu Tyr  Cys Ala Gly Tyr Gln  Gly Glu Asp Thr Leu  Leu Val Met
    1235                 1240                 1245

ttt tat  aac caa caa gac aca  cta gat agt tat aaa  aac gct tca      3789
Phe Tyr  Asn Gln Gln Asp Thr  Leu Asp Ser Tyr Lys  Asn Ala Ser
    1250                 1255                 1260

atg caa  gga cta tat atc ttt  gct gat atg gca tcc  aaa gat atg      3834
Met Gln  Gly Leu Tyr Ile Phe  Ala Asp Met Ala Ser  Lys Asp Met
    1265                 1270                 1275

acc cca  gaa cag agc aat gtt  tat cgg gat aat agc  tat caa caa      3879
Thr Pro  Glu Gln Ser Asn Val  Tyr Arg Asp Asn Ser  Tyr Gln Gln
    1280                 1285                 1290

ttt gat  acc aat aat gtc aga  aga gtg aat aac cgc  tat gca gag      3924
Phe Asp  Thr Asn Asn Val Arg  Arg Val Asn Asn Arg  Tyr Ala Glu
    1295                 1300                 1305

gat tat  gag att cct tcc tcg  gta agt agc cgt aaa  gac tat ggt      3969
Asp Tyr  Glu Ile Pro Ser Ser  Val Ser Ser Arg Lys  Asp Tyr Gly
    1310                 1315                 1320

tgg gga  gat tat tac ctc agc  atg gta tat aac gga  gat att cca      4014
Trp Gly  Asp Tyr Tyr Leu Ser  Met Val Tyr Asn Gly  Asp Ile Pro
    1325                 1330                 1335

act atc  aat tac aaa gcc gca  tca agt gat tta aaa  atc tat atc      4059
Thr Ile  Asn Tyr Lys Ala Ala  Ser Ser Asp Leu Lys  Ile Tyr Ile
    1340                 1345                 1350

tca cca  aaa tta aga att att  cat aat gga tat gaa  gga cag aag      4104
Ser Pro  Lys Leu Arg Ile Ile  His Asn Gly Tyr Glu  Gly Gln Lys
    1355                 1360                 1365

cgc aat  caa tgc aat ctg atg  aat aaa tat ggc aaa  cta ggt gat      4149
Arg Asn  Gln Cys Asn Leu Met  Asn Lys Tyr Gly Lys  Leu Gly Asp
    1370                 1375                 1380

aaa ttt  att gtt tat act agc  ttg ggg gtc aat cca  aat aac tcg      4194
Lys Phe  Ile Val Tyr Thr Ser  Leu Gly Val Asn Pro  Asn Asn Ser
    1385                 1390                 1395

tca aat  aag ctc atg ttt tac  ccc gtc tat caa tat  agc gga aac      4239
Ser Asn  Lys Leu Met Phe Tyr  Pro Val Tyr Gln Tyr  Ser Gly Asn
    1400                 1405                 1410

acc agt  gga ctc aat caa ggg  aga cta cta ttc cac  cgt gac acc      4284
Thr Ser  Gly Leu Asn Gln Gly  Arg Leu Leu Phe His  Arg Asp Thr
    1415                 1420                 1425

act tat  cca tct aaa gta gaa  gct tgg att cct gga  gca aaa cgt      4329
Thr Tyr  Pro Ser Lys Val Glu  Ala Trp Ile Pro Gly  Ala Lys Arg
    1430                 1435                 1440

tct cta  acc aac caa aat gcc  gcc att ggt gat gat  tat gct aca      4374
Ser Leu  Thr Asn Gln Asn Ala  Ala Ile Gly Asp Asp  Tyr Ala Thr
    1445                 1450                 1455

gac tct  ctg aat aaa ccg gat  gat ctt aag caa tat  atc ttt atg      4419
Asp Ser  Leu Asn Lys Pro Asp  Asp Leu Lys Gln Tyr  Ile Phe Met
    1460                 1465                 1470

act gac  agt aaa ggg act gct  act gat gtc tca ggc  cca gta gag      4464
Thr Asp  Ser Lys Gly Thr Ala  Thr Asp Val Ser Gly  Pro Val Glu
    1475                 1480                 1485
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att aat  act gca att tct cca  gca aaa gtt cag ata  ata gtc aaa      4509
Ile Asn  Thr Ala Ile Ser Pro  Ala Lys Val Gln Ile  Ile Val Lys
    1490                 1495                 1500

gcg ggt  ggc aag gag caa act  ttt acc gca gat aaa  gat gtc tcc      4554
Ala Gly  Gly Lys Glu Gln Thr  Phe Thr Ala Asp Lys  Asp Val Ser
    1505                 1510                 1515

att cag  cca tca cct agc ttt  gat gaa atg aat tat  caa ttt aat      4599
Ile Gln  Pro Ser Pro Ser Phe  Asp Glu Met Asn Tyr  Gln Phe Asn
    1520                 1525                 1530

gcc ctt  gaa ata gac ggt tct  ggt ctg aat ttt att  aac aac tca      4644
Ala Leu  Glu Ile Asp Gly Ser  Gly Leu Asn Phe Ile  Asn Asn Ser
    1535                 1540                 1545

gcc agt  att gat gtt act ttt  acc gca ttt gcg gag  gat ggc cgc      4689
Ala Ser  Ile Asp Val Thr Phe  Thr Ala Phe Ala Glu  Asp Gly Arg
    1550                 1555                 1560

aaa ctg  ggt tat gaa agt ttc  agt att cct gtt acc  ctc aag gta      4734
Lys Leu  Gly Tyr Glu Ser Phe  Ser Ile Pro Val Thr  Leu Lys Val
    1565                 1570                 1575

agt acc  gat aat gcc ctg acc  ctg cac cat aat gaa  aat ggt gcg      4779
Ser Thr  Asp Asn Ala Leu Thr  Leu His His Asn Glu  Asn Gly Ala
    1580                 1585                 1590

caa tat  atg caa tgg caa tcc  tat cgt acc cgc ctg  aat act cta      4824
Gln Tyr  Met Gln Trp Gln Ser  Tyr Arg Thr Arg Leu  Asn Thr Leu
    1595                 1600                 1605

ttt gcc  cgc cag ttg gtt gca  cgc gcc acc acc gga  atc gat aca      4869
Phe Ala  Arg Gln Leu Val Ala  Arg Ala Thr Thr Gly  Ile Asp Thr
    1610                 1615                 1620

att ctg  agt atg gaa act cag  aat att cag gaa ccg  cag tta ggc      4914
Ile Leu  Ser Met Glu Thr Gln  Asn Ile Gln Glu Pro  Gln Leu Gly
    1625                 1630                 1635

aaa ggt  ttc tat gct acg ttc  gtg ata cct ccc tat  aac cta tca      4959
Lys Gly  Phe Tyr Ala Thr Phe  Val Ile Pro Pro Tyr  Asn Leu Ser
    1640                 1645                 1650

act cat  ggt gat gaa cgt tgg  ttt aag ctt tat atc  aaa cat gtt      5004
Thr His  Gly Asp Glu Arg Trp  Phe Lys Leu Tyr Ile  Lys His Val
    1655                 1660                 1665

gtt gat  aat aat tca cat att  atc tat tca ggc cag  cta aca gat      5049
Val Asp  Asn Asn Ser His Ile  Ile Tyr Ser Gly Gln  Leu Thr Asp
    1670                 1675                 1680

aca aat  ata aac atc aca tta  ttt att cct ctt gat  gat gtc cca      5094
Thr Asn  Ile Asn Ile Thr Leu  Phe Ile Pro Leu Asp  Asp Val Pro
    1685                 1690                 1695

ttg aat  caa gat tat cac gcc  aag gtt tat atg acc  ttc aag aaa      5139
Leu Asn  Gln Asp Tyr His Ala  Lys Val Tyr Met Thr  Phe Lys Lys
    1700                 1705                 1710

tca cca  tca gat ggt acc tgg  tgg ggc cct cac ttt  gtt aga gat      5184
Ser Pro  Ser Asp Gly Thr Trp  Trp Gly Pro His Phe  Val Arg Asp
    1715                 1720                 1725

gat aaa  gga ata gta aca ata  aac cct aaa tcc att  ttg acc cat      5229
Asp Lys  Gly Ile Val Thr Ile  Asn Pro Lys Ser Ile  Leu Thr His
    1730                 1735                 1740

ttt gag  agc gtc aat gtc ctg  aat aat att agt agc  gaa cca atg      5274
Phe Glu  Ser Val Asn Val Leu  Asn Asn Ile Ser Ser  Glu Pro Met
    1745                 1750                 1755

gat ttc  agc ggc gct aac agc  ctc tat ttc tgg gaa  ctg ttc tac      5319
Asp Phe  Ser Gly Ala Asn Ser  Leu Tyr Phe Trp Glu  Leu Phe Tyr
    1760                 1765                 1770

tat acc  ccg atg ctg gtt gct  caa cgt ttg ctg cat  gaa cag aac      5364
Tyr Thr  Pro Met Leu Val Ala  Gln Arg Leu Leu His  Glu Gln Asn
    1775                 1780                 1785
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ttc gat  gaa gcc aac cgt tgg  ctg aaa tat gtc tgg  agt cca tcc      5409
Phe Asp  Glu Ala Asn Arg Trp  Leu Lys Tyr Val Trp  Ser Pro Ser
    1790                 1795                 1800

ggt tat  att gtc cac ggc cag  att cag aac tac cag  tgg aac gtc      5454
Gly Tyr  Ile Val His Gly Gln  Ile Gln Asn Tyr Gln  Trp Asn Val
    1805                 1810                 1815

cgc ccg  tta ctg gaa gac acc  agt tgg aac agt gat  cct ttg gat      5499
Arg Pro  Leu Leu Glu Asp Thr  Ser Trp Asn Ser Asp  Pro Leu Asp
    1820                 1825                 1830

tcc gtc  gat cct gac gcg gta  gca cag cac gat cca  atg cac tac      5544
Ser Val  Asp Pro Asp Ala Val  Ala Gln His Asp Pro  Met His Tyr
    1835                 1840                 1845

aaa gtt  tca act ttt atg cgt  acc ttg gat cta ttg  ata gca cgc      5589
Lys Val  Ser Thr Phe Met Arg  Thr Leu Asp Leu Leu  Ile Ala Arg
    1850                 1855                 1860

ggc gac  cat gct tat cgc caa  ctg gaa cga gat aca  ctc aac gaa      5634
Gly Asp  His Ala Tyr Arg Gln  Leu Glu Arg Asp Thr  Leu Asn Glu
    1865                 1870                 1875

gcg aag  atg tgg tat atg caa  gcg ctg cat cta tta  ggt gac aaa      5679
Ala Lys  Met Trp Tyr Met Gln  Ala Leu His Leu Leu  Gly Asp Lys
    1880                 1885                 1890

cct tat  cta ccg ctg agt acg  aca tgg agt gat cca  cga cta gac      5724
Pro Tyr  Leu Pro Leu Ser Thr  Thr Trp Ser Asp Pro  Arg Leu Asp
    1895                 1900                 1905

aga gcc  gcg gat atc act acc  caa aat gct cac gac  agc gca ata      5769
Arg Ala  Ala Asp Ile Thr Thr  Gln Asn Ala His Asp  Ser Ala Ile
    1910                 1915                 1920

gtc gct  ctg cgg cag aat ata  cct aca ccg gca cct  tta tca ttg      5814
Val Ala  Leu Arg Gln Asn Ile  Pro Thr Pro Ala Pro  Leu Ser Leu
    1925                 1930                 1935

cgc agc  gct aat acc ctg act  gat ctc ttc ctg ccg  caa atc aat      5859
Arg Ser  Ala Asn Thr Leu Thr  Asp Leu Phe Leu Pro  Gln Ile Asn
    1940                 1945                 1950

gaa gtg  atg atg aat tac tgg  cag aca tta gct cag  aga gta tac      5904
Glu Val  Met Met Asn Tyr Trp  Gln Thr Leu Ala Gln  Arg Val Tyr
    1955                 1960                 1965

aat ctg  cgt cat aac ctc tct  atc gac ggc cag ccg  tta tat ctg      5949
Asn Leu  Arg His Asn Leu Ser  Ile Asp Gly Gln Pro  Leu Tyr Leu
    1970                 1975                 1980

cca atc  tat gcc aca ccg gcc  gat ccg aaa gcg tta  ctc agc gcc      5994
Pro Ile  Tyr Ala Thr Pro Ala  Asp Pro Lys Ala Leu  Leu Ser Ala
    1985                 1990                 1995

gcc gtt  gcc act tct caa ggt  gga ggc aag cta ccg  gaa tca ttt      6039
Ala Val  Ala Thr Ser Gln Gly  Gly Gly Lys Leu Pro  Glu Ser Phe
    2000                 2005                 2010

atg tcc  ctg tgg cgt ttc ccg  cac atg ctg gaa aat  gcg cgc ggc      6084
Met Ser  Leu Trp Arg Phe Pro  His Met Leu Glu Asn  Ala Arg Gly
    2015                 2020                 2025

atg gtt  agc cag ctc acc cag  ttc ggc tcc acg tta  caa aat att      6129
Met Val  Ser Gln Leu Thr Gln  Phe Gly Ser Thr Leu  Gln Asn Ile
    2030                 2035                 2040

atc gaa  cgt cag gac gcg gaa  gcg ctc aat gcg tta  tta caa aat      6174
Ile Glu  Arg Gln Asp Ala Glu  Ala Leu Asn Ala Leu  Leu Gln Asn
    2045                 2050                 2055

cag gcc  gcc gag ctg ata ttg  act aac ctg agc att  cag gac aaa      6219
Gln Ala  Ala Glu Leu Ile Leu  Thr Asn Leu Ser Ile  Gln Asp Lys
    2060                 2065                 2070

acc att  gaa gaa ttg gat gcc  gag aaa acg gtg ttg  gaa aaa tcc      6264
Thr Ile  Glu Glu Leu Asp Ala  Glu Lys Thr Val Leu  Glu Lys Ser
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    2075                2080                2085

aaa gcg  gga gca caa tcg cgc  ttt gat agc tac ggc  aaa ctg tac      6309
Lys Ala  Gly Ala Gln Ser Arg  Phe Asp Ser Tyr Gly  Lys Leu Tyr
    2090                2095                2100

gat gag  aat atc aac gcc ggt  gaa aac caa gcc atg  acg cta cga      6354
Asp Glu  Asn Ile Asn Ala Gly  Glu Asn Gln Ala Met  Thr Leu Arg
    2105                2110                2115

gcg tcc  gcc gcc ggg ctt acc  acg gca gtt cag gca  tcc cgt ctg      6399
Ala Ser  Ala Ala Gly Leu Thr  Thr Ala Val Gln Ala  Ser Arg Leu
    2120                2125                2130

gcc ggt  gcg gcg gct gat ctg  gtg cct aac atc ttc  ggc ttt gcc      6444
Ala Gly  Ala Ala Ala Asp Leu  Val Pro Asn Ile Phe  Gly Phe Ala
    2135                2140                2145

ggt ggc  ggc agc cgt tgg ggg  gct atc gct gag gcg  aca ggt tat      6489
Gly Gly  Gly Ser Arg Trp Gly  Ala Ile Ala Glu Ala  Thr Gly Tyr
    2150                2155                2160

gtg atg  gaa ttc tcc gcg aat  gtt atg aac acc gaa  gcg gat aaa      6534
Val Met  Glu Phe Ser Ala Asn  Val Met Asn Thr Glu  Ala Asp Lys
    2165                2170                2175

att agc  caa tct gaa acc tac  cgt cgt cgc cgt cag  gag tgg gag      6579
Ile Ser  Gln Ser Glu Thr Tyr  Arg Arg Arg Arg Gln  Glu Trp Glu
    2180                2185                2190

atc cag  cgg aat aat gcc gaa  gcg gaa ttg aag caa  atc gat gct      6624
Ile Gln  Arg Asn Asn Ala Glu  Ala Glu Leu Lys Gln  Ile Asp Ala
    2195                2200                2205

cag ctc  aaa tca ctc gct gta  cgc cgc gaa gcc gcc  gta ttg cag      6669
Gln Leu  Lys Ser Leu Ala Val  Arg Arg Glu Ala Ala  Val Leu Gln
    2210                2215                2220

aaa acc  agt ctg aaa acc caa  caa gaa cag acc caa  tct caa ttg      6714
Lys Thr  Ser Leu Lys Thr Gln  Gln Glu Gln Thr Gln  Ser Gln Leu
    2225                2230                2235

gcc ttc  ctg caa cgt aag ttc  agc aat cag gcg tta  tac aac tgg      6759
Ala Phe  Leu Gln Arg Lys Phe  Ser Asn Gln Ala Leu  Tyr Asn Trp
    2240                2245                2250

ctg cgt  ggt cga ctg gcg gcg  att tac ttc cag ttc  tac gat ttg      6804
Leu Arg  Gly Arg Leu Ala Ala  Ile Tyr Phe Gln Phe  Tyr Asp Leu
    2255                2260                2265

gcc gtc  gcg cgt tgc ctg atg  gca gaa caa gct tac  cgt tgg gaa      6849
Ala Val  Ala Arg Cys Leu Met  Ala Glu Gln Ala Tyr  Arg Trp Glu
    2270                2275                2280

ctc aat  gat gac tct gcc cgc  ttc att aaa ccg ggc  gcc tgg cag      6894
Leu Asn  Asp Asp Ser Ala Arg  Phe Ile Lys Pro Gly  Ala Trp Gln
    2285                2290                2295

gga acc  tat gcc ggt ctg ctt  gca ggt gaa acc ttg  atg ctg agt      6939
Gly Thr  Tyr Ala Gly Leu Leu  Ala Gly Glu Thr Leu  Met Leu Ser
    2300                2305                2310

ctg gca  caa atg gaa gac gct  cat ctg aaa cgc gat  aaa cgc gca      6984
Leu Ala  Gln Met Glu Asp Ala  His Leu Lys Arg Asp  Lys Arg Ala
    2315                2320                2325

tta gag  gtt gaa cgc aca gta  tcg ctg gcc gaa gtt  tat gca gga      7029
Leu Glu  Val Glu Arg Thr Val  Ser Leu Ala Glu Val  Tyr Ala Gly
    2330                2335                2340

tta cca  aaa gat aac ggt cca  ttt tcc ctg gct cag  gaa att gac      7074
Leu Pro  Lys Asp Asn Gly Pro  Phe Ser Leu Ala Gln  Glu Ile Asp
    2345                2350                2355

aag ctg  gtg agt caa ggt tca  ggc agt gcc ggc agt  ggt aat aat      7119
Lys Leu  Val Ser Gln Gly Ser  Gly Ser Ala Gly Ser  Gly Asn Asn
    2360                2365                2370

aat ttg  gcg ttc ggc gcc ggc  acg gac act aaa acc  tct ttg cag      7164
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Asn Leu  Ala Phe Gly Ala Gly  Thr Asp Thr Lys Thr  Ser Leu Gln
    2375                 2380                 2385

gca tca  gtt tca ttc gct gat  ttg aaa att cgt gaa  gat tac ccg      7209
Ala Ser  Val Ser Phe Ala Asp  Leu Lys Ile Arg Glu  Asp Tyr Pro
    2390                 2395                 2400

gca tcg  ctt ggc aaa att cga  cgt atc aaa cag atc  agc gtc act      7254
Ala Ser  Leu Gly Lys Ile Arg  Arg Ile Lys Gln Ile  Ser Val Thr
    2405                 2410                 2415

ttg ccc  gcg cta ctg gga ccg  tat cag gat gta cag  gca ata ttg      7299
Leu Pro  Ala Leu Leu Gly Pro  Tyr Gln Asp Val Gln  Ala Ile Leu
    2420                 2425                 2430

tct tac  ggc gat aaa gcc gga  tta gct aac ggc tgt  gaa gcg ctg      7344
Ser Tyr  Gly Asp Lys Ala Gly  Leu Ala Asn Gly Cys  Glu Ala Leu
    2435                 2440                 2445

gca gtt  tct cac ggt atg aat  gac agc ggc caa ttc  cag ctc gat      7389
Ala Val  Ser His Gly Met Asn  Asp Ser Gly Gln Phe  Gln Leu Asp
    2450                 2455                 2460

ttc aac  gat ggc aaa ttc ctg  cca ttc gaa ggc atc  gcc att gat      7434
Phe Asn  Asp Gly Lys Phe Leu  Pro Phe Glu Gly Ile  Ala Ile Asp
    2465                 2470                 2475

caa ggc  acg ctg aca ctg agc  ttc cca aat gca tct  atg ccg gag      7479
Gln Gly  Thr Leu Thr Leu Ser  Phe Pro Asn Ala Ser  Met Pro Glu
    2480                 2485                 2490

aaa ggt  aaa caa gcc act atg  tta aaa acc ctg aac  gat atc att      7524
Lys Gly  Lys Gln Ala Thr Met  Leu Lys Thr Leu Asn  Asp Ile Ile
    2495                 2500                 2505

ttg cat  att cgc tac acc att  aaa taa                               7551
Leu His  Ile Arg Tyr Thr Ile  Lys
    2510                 2515


<210> SEQ ID NO 2
<211> LENGTH: 2516
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 2

Met Asn Glu Ser Val Lys Glu Ile Pro Asp Val Leu Lys Ser Gln Cys
1               5                   10                  15

Gly Phe Asn Cys Leu Thr Asp Ile Ser His Ser Ser Phe Asn Glu Phe
            20                  25                  30

Arg Gln Gln Val Ser Glu His Leu Ser Trp Ser Glu Thr His Asp Leu
        35                  40                  45

Tyr His Asp Ala Gln Gln Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala
    50                  55                  60

Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65                  70                  75                  80

Ala Ile Leu Ala Pro Asn Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe
                85                  90                  95

Ser Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Thr Val Ser Ser Met
            100                 105                 110

Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
        115                 120                 125

Leu His Ala Ser Asp Ser Val Tyr Tyr Leu Asp Thr Arg Arg Pro Asp
    130                 135                 140

Leu Lys Ser Met Ala Leu Ser Gln Gln Asn Met Asp Ile Glu Leu Ser
145                 150                 155                 160

Thr Leu Ser Leu Ser Asn Glu Leu Leu Leu Glu Ser Ile Lys Thr Glu
                165                 170                 175
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Ser Lys Leu Glu Asn Tyr Thr Lys Val Met Glu Met Leu Ser Thr Phe
            180                 185                 190

Arg Pro Ser Gly Ala Thr Pro Tyr His Asp Ala Tyr Glu Asn Val Arg
        195                 200                 205

Glu Val Ile Gln Leu Gln Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser
    210                 215                 220

Pro Ala Ile Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile Asn
225                 230                 235                 240

Ala Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr
                245                 250                 255

Glu Gly Asn Ala Glu Glu Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu
            260                 265                 270

Pro Ala Ser Leu Ala Met Pro Glu Tyr Leu Lys Arg Tyr Tyr Asn Leu
        275                 280                 285

Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly
    290                 295                 300

Gln Gln Glu Tyr Ser Asn Asn Gln Leu Ile Thr Pro Val Val Asn Ser
305                 310                 315                 320

Ser Asp Gly Thr Val Lys Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr
                325                 330                 335

Asn Ala Tyr Gln Met Asp Val Glu Leu Phe Pro Phe Gly Gly Glu Asn
            340                 345                 350

Tyr Arg Leu Asp Tyr Lys Phe Lys Asn Phe Tyr Asn Ala Ser Tyr Leu
        355                 360                 365

Ser Ile Lys Leu Asn Asp Lys Arg Glu Leu Val Arg Thr Glu Gly Ala
    370                 375                 380

Pro Gln Val Asn Ile Glu Tyr Ser Ala Asn Ile Thr Leu Asn Thr Ala
385                 390                 395                 400

Asp Ile Ser Gln Pro Phe Glu Ile Gly Leu Thr Arg Val Leu Pro Ser
                405                 410                 415

Gly Ser Trp Ala Tyr Ala Ala Ala Lys Phe Thr Val Glu Glu Tyr Asn
            420                 425                 430

Gln Tyr Ser Phe Leu Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg
        435                 440                 445

Ala Thr Glu Leu Ser Pro Thr Ile Leu Glu Gly Ile Val Arg Ser Val
    450                 455                 460

Asn Leu Gln Leu Asp Ile Asn Thr Asp Val Leu Gly Lys Val Phe Leu
465                 470                 475                 480

Thr Lys Tyr Tyr Met Gln Arg Tyr Ala Ile His Ala Glu Thr Ala Leu
                485                 490                 495

Ile Leu Cys Asn Ala Pro Ile Ser Gln Arg Ser Tyr Asp Asn Gln Pro
            500                 505                 510

Ser Gln Phe Asp Arg Leu Phe Asn Thr Pro Leu Leu Asn Gly Gln Tyr
        515                 520                 525

Phe Ser Thr Gly Asp Glu Glu Ile Asp Leu Asn Ser Gly Ser Thr Gly
    530                 535                 540

Asp Trp Arg Lys Thr Ile Leu Lys Arg Ala Phe Asn Ile Asp Asp Val
545                 550                 555                 560

Ser Leu Phe Arg Leu Leu Lys Ile Thr Asp His Asp Asn Lys Asp Gly
                565                 570                 575

Lys Ile Lys Asn Asn Leu Lys Asn Leu Ser Asn Leu Tyr Ile Gly Lys
            580                 585                 590
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Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Asp Leu Leu
        595                 600                 605

Leu Ile Ala Val Gly Glu Gly Lys Thr Asn Leu Ser Ala Ile Ser Asp
    610                 615                 620

Lys Gln Leu Ala Thr Leu Ile Arg Lys Leu Asn Thr Ile Thr Ser Trp
625                 630                 635                 640

Leu His Thr Gln Lys Trp Ser Val Phe Gln Leu Phe Ile Met Thr Ser
                645                 650                 655

Thr Ser Tyr Asn Lys Thr Leu Thr Pro Glu Ile Lys Asn Leu Leu Asp
            660                 665                 670

Thr Val Tyr His Gly Leu Gln Gly Phe Asp Lys Asp Lys Ala Asp Leu
        675                 680                 685

Leu His Val Met Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Ser Ser
    690                 695                 700

Glu Asn Val Ala His Ser Val Leu Leu Trp Ala Asp Lys Leu Gln Pro
705                 710                 715                 720

Gly Asp Gly Ala Met Thr Ala Glu Lys Phe Trp Asp Trp Leu Asn Thr
                725                 730                 735

Lys Tyr Thr Pro Gly Ser Ser Glu Ala Val Glu Thr Gln Glu His Ile
            740                 745                 750

Val Gln Tyr Cys Gln Ala Leu Ala Gln Leu Glu Met Val Tyr His Ser
        755                 760                 765

Thr Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Val Thr Lys Pro Glu
    770                 775                 780

Met Phe Gly Ala Ala Thr Gly Ala Ala Pro Ala His Asp Ala Leu Ser
785                 790                 795                 800

Leu Ile Met Leu Thr Arg Phe Ala Asp Trp Val Asn Ala Leu Gly Glu
                805                 810                 815

Lys Ala Ser Ser Val Leu Ala Ala Phe Glu Ala Asn Ser Leu Thr Ala
            820                 825                 830

Glu Gln Leu Ala Asp Ala Met Asn Leu Asp Ala Asn Leu Leu Leu Gln
        835                 840                 845

Ala Ser Ile Gln Ala Gln Asn His Gln His Leu Pro Pro Val Thr Pro
    850                 855                 860

Glu Asn Ala Phe Ser Cys Trp Thr Ser Ile Asn Thr Ile Leu Gln Trp
865                 870                 875                 880

Val Asn Val Ala Gln Gln Leu Asn Val Ala Pro Gln Gly Val Ser Ala
                885                 890                 895

Leu Val Gly Leu Asp Tyr Ile Gln Ser Met Lys Glu Thr Pro Thr Tyr
            900                 905                 910

Ala Gln Trp Glu Asn Ala Ala Gly Val Leu Thr Ala Gly Leu Asn Ser
        915                 920                 925

Gln Gln Ala Asn Thr Leu His Ala Phe Leu Asp Glu Ser Arg Ser Ala
    930                 935                 940

Ala Leu Ser Thr Tyr Tyr Ile Arg Gln Val Ala Lys Ala Ala Ala Ala
945                 950                 955                 960

Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln
                965                 970                 975

Val Ser Ala Ala Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser
            980                 985                 990

Ile Gln Leu Tyr Val Asn Arg Ala  Leu Glu Asn Val Glu  Glu Asn Ala
        995                  1000                1005

Asn Ser  Gly Val Ile Ser Arg  Gln Phe Phe Ile Asp  Trp Asp Lys
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    1010                1015                1020

Tyr Asn  Lys Arg Tyr Ser Thr  Trp Ala Gly Val Ser  Gln Leu Val
    1025                1030                1035

Tyr Tyr  Pro Glu Asn Tyr Ile  Asp Pro Thr Met Arg  Ile Gly Gln
    1040                1045                1050

Thr Lys  Met Met Asp Ala Leu  Leu Gln Ser Val Ser  Gln Ser Gln
    1055                1060                1065

Leu Asn  Ala Asp Thr Val Glu  Asp Ala Phe Met Ser  Tyr Leu Thr
    1070                1075                1080

Ser Phe  Glu Gln Val Ala Asn  Leu Lys Val Ile Ser  Ala Tyr His
    1085                1090                1095

Asp Asn  Ile Asn Asn Asp Gln  Gly Leu Thr Tyr Phe  Ile Gly Leu
    1100                1105                1110

Ser Glu  Thr Asp Ala Gly Glu  Tyr Tyr Trp Arg Ser  Val Asp His
    1115                1120                1125

Ser Lys  Phe Asn Asp Gly Lys  Phe Ala Ala Asn Ala  Trp Ser Glu
    1130                1135                1140

Trp His  Lys Ile Asp Cys Pro  Ile Asn Pro Tyr Lys  Ser Thr Ile
    1145                1150                1155

Arg Pro  Val Ile Tyr Lys Ser  Arg Leu Tyr Leu Leu  Trp Leu Glu
    1160                1165                1170

Gln Lys  Glu Ile Thr Lys Gln  Thr Gly Asn Ser Lys  Asp Gly Tyr
    1175                1180                1185

Gln Thr  Glu Thr Asp Tyr Arg  Tyr Glu Leu Lys Leu  Ala His Ile
    1190                1195                1200

Arg Tyr  Asp Gly Thr Trp Asn  Thr Pro Ile Thr Phe  Asp Val Asn
    1205                1210                1215

Lys Lys  Ile Ser Glu Leu Lys  Leu Glu Lys Asn Arg  Ala Pro Gly
    1220                1225                1230

Leu Tyr  Cys Ala Gly Tyr Gln  Gly Glu Asp Thr Leu  Leu Val Met
    1235                1240                1245

Phe Tyr  Asn Gln Gln Asp Thr  Leu Asp Ser Tyr Lys  Asn Ala Ser
    1250                1255                1260

Met Gln  Gly Leu Tyr Ile Phe  Ala Asp Met Ala Ser  Lys Asp Met
    1265                1270                1275

Thr Pro  Glu Gln Ser Asn Val  Tyr Arg Asp Asn Ser  Tyr Gln Gln
    1280                1285                1290

Phe Asp  Thr Asn Asn Val Arg  Arg Val Asn Asn Arg  Tyr Ala Glu
    1295                1300                1305

Asp Tyr  Glu Ile Pro Ser Ser  Val Ser Ser Arg Lys  Asp Tyr Gly
    1310                1315                1320

Trp Gly  Asp Tyr Tyr Leu Ser  Met Val Tyr Asn Gly  Asp Ile Pro
    1325                1330                1335

Thr Ile  Asn Tyr Lys Ala Ala  Ser Ser Asp Leu Lys  Ile Tyr Ile
    1340                1345                1350

Ser Pro  Lys Leu Arg Ile Ile  His Asn Gly Tyr Glu  Gly Gln Lys
    1355                1360                1365

Arg Asn  Gln Cys Asn Leu Met  Asn Lys Tyr Gly Lys  Leu Gly Asp
    1370                1375                1380

Lys Phe  Ile Val Tyr Thr Ser  Leu Gly Val Asn Pro  Asn Asn Ser
    1385                1390                1395

Ser Asn  Lys Leu Met Phe Tyr  Pro Val Tyr Gln Tyr  Ser Gly Asn
    1400                1405                1410
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Thr Ser  Gly Leu Asn Gln Gly  Arg Leu Leu Phe His  Arg Asp Thr
    1415                 1420                 1425

Thr Tyr  Pro Ser Lys Val Glu  Ala Trp Ile Pro Gly  Ala Lys Arg
    1430                 1435                 1440

Ser Leu  Thr Asn Gln Asn Ala  Ala Ile Gly Asp Asp  Tyr Ala Thr
    1445                 1450                 1455

Asp Ser  Leu Asn Lys Pro Asp  Asp Leu Lys Gln Tyr  Ile Phe Met
    1460                 1465                 1470

Thr Asp  Ser Lys Gly Thr Ala  Thr Asp Val Ser Gly  Pro Val Glu
    1475                 1480                 1485

Ile Asn  Thr Ala Ile Ser Pro  Ala Lys Val Gln Ile  Ile Val Lys
    1490                 1495                 1500

Ala Gly  Gly Lys Glu Gln Thr  Phe Thr Ala Asp Lys  Asp Val Ser
    1505                 1510                 1515

Ile Gln  Pro Ser Pro Ser Phe  Asp Glu Met Asn Tyr  Gln Phe Asn
    1520                 1525                 1530

Ala Leu  Glu Ile Asp Gly Ser  Gly Leu Asn Phe Ile  Asn Asn Ser
    1535                 1540                 1545

Ala Ser  Ile Asp Val Thr Phe  Thr Ala Phe Ala Glu  Asp Gly Arg
    1550                 1555                 1560

Lys Leu  Gly Tyr Glu Ser Phe  Ser Ile Pro Val Thr  Leu Lys Val
    1565                 1570                 1575

Ser Thr  Asp Asn Ala Leu Thr  Leu His His Asn Glu  Asn Gly Ala
    1580                 1585                 1590

Gln Tyr  Met Gln Trp Gln Ser  Tyr Arg Thr Arg Leu  Asn Thr Leu
    1595                 1600                 1605

Phe Ala  Arg Gln Leu Val Ala  Arg Ala Thr Thr Gly  Ile Asp Thr
    1610                 1615                 1620

Ile Leu  Ser Met Glu Thr Gln  Asn Ile Gln Glu Pro  Gln Leu Gly
    1625                 1630                 1635

Lys Gly  Phe Tyr Ala Thr Phe  Val Ile Pro Pro Tyr  Asn Leu Ser
    1640                 1645                 1650

Thr His  Gly Asp Glu Arg Trp  Phe Lys Leu Tyr Ile  Lys His Val
    1655                 1660                 1665

Val Asp  Asn Asn Ser His Ile  Ile Tyr Ser Gly Gln  Leu Thr Asp
    1670                 1675                 1680

Thr Asn  Ile Asn Ile Thr Leu  Phe Ile Pro Leu Asp  Asp Val Pro
    1685                 1690                 1695

Leu Asn  Gln Asp Tyr His Ala  Lys Val Tyr Met Thr  Phe Lys Lys
    1700                 1705                 1710

Ser Pro  Ser Asp Gly Thr Trp  Trp Gly Pro His Phe  Val Arg Asp
    1715                 1720                 1725

Asp Lys  Gly Ile Val Thr Ile  Asn Pro Lys Ser Ile  Leu Thr His
    1730                 1735                 1740

Phe Glu  Ser Val Asn Val Leu  Asn Asn Ile Ser Ser  Glu Pro Met
    1745                 1750                 1755

Asp Phe  Ser Gly Ala Asn Ser  Leu Tyr Phe Trp Glu  Leu Phe Tyr
    1760                 1765                 1770

Tyr Thr  Pro Met Leu Val Ala  Gln Arg Leu Leu His  Glu Gln Asn
    1775                 1780                 1785

Phe Asp  Glu Ala Asn Arg Trp  Leu Lys Tyr Val Trp  Ser Pro Ser
    1790                 1795                 1800
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Gly Tyr  Ile Val His Gly Gln  Ile Gln Asn Tyr Gln  Trp Asn Val
    1805                 1810                 1815

Arg Pro  Leu Leu Glu Asp Thr  Ser Trp Asn Ser Asp  Pro Leu Asp
    1820                 1825                 1830

Ser Val  Asp Pro Asp Ala Val  Ala Gln His Asp Pro  Met His Tyr
    1835                 1840                 1845

Lys Val  Ser Thr Phe Met Arg  Thr Leu Asp Leu Leu  Ile Ala Arg
    1850                 1855                 1860

Gly Asp  His Ala Tyr Arg Gln  Leu Glu Arg Asp Thr  Leu Asn Glu
    1865                 1870                 1875

Ala Lys  Met Trp Tyr Met Gln  Ala Leu His Leu Leu  Gly Asp Lys
    1880                 1885                 1890

Pro Tyr  Leu Pro Leu Ser Thr  Thr Trp Ser Asp Pro  Arg Leu Asp
    1895                 1900                 1905

Arg Ala  Ala Asp Ile Thr Thr  Gln Asn Ala His Asp  Ser Ala Ile
    1910                 1915                 1920

Val Ala  Leu Arg Gln Asn Ile  Pro Thr Pro Ala Pro  Leu Ser Leu
    1925                 1930                 1935

Arg Ser  Ala Asn Thr Leu Thr  Asp Leu Phe Leu Pro  Gln Ile Asn
    1940                 1945                 1950

Glu Val  Met Met Asn Tyr Trp  Gln Thr Leu Ala Gln  Arg Val Tyr
    1955                 1960                 1965

Asn Leu  Arg His Asn Leu Ser  Ile Asp Gly Gln Pro  Leu Tyr Leu
    1970                 1975                 1980

Pro Ile  Tyr Ala Thr Pro Ala  Asp Pro Lys Ala Leu  Leu Ser Ala
    1985                 1990                 1995

Ala Val  Ala Thr Ser Gln Gly  Gly Gly Lys Leu Pro  Glu Ser Phe
    2000                 2005                 2010

Met Ser  Leu Trp Arg Phe Pro  His Met Leu Glu Asn  Ala Arg Gly
    2015                 2020                 2025

Met Val  Ser Gln Leu Thr Gln  Phe Gly Ser Thr Leu  Gln Asn Ile
    2030                 2035                 2040

Ile Glu  Arg Gln Asp Ala Glu  Ala Leu Asn Ala Leu  Leu Gln Asn
    2045                 2050                 2055

Gln Ala  Ala Glu Leu Ile Leu  Thr Asn Leu Ser Ile  Gln Asp Lys
    2060                 2065                 2070

Thr Ile  Glu Glu Leu Asp Ala  Glu Lys Thr Val Leu  Glu Lys Ser
    2075                 2080                 2085

Lys Ala  Gly Ala Gln Ser Arg  Phe Asp Ser Tyr Gly  Lys Leu Tyr
    2090                 2095                 2100

Asp Glu  Asn Ile Asn Ala Gly  Glu Asn Gln Ala Met  Thr Leu Arg
    2105                 2110                 2115

Ala Ser  Ala Ala Gly Leu Thr  Thr Ala Val Gln Ala  Ser Arg Leu
    2120                 2125                 2130

Ala Gly  Ala Ala Ala Asp Leu  Val Pro Asn Ile Phe  Gly Phe Ala
    2135                 2140                 2145

Gly Gly  Gly Ser Arg Trp Gly  Ala Ile Ala Glu Ala  Thr Gly Tyr
    2150                 2155                 2160

Val Met  Glu Phe Ser Ala Asn  Val Met Asn Thr Glu  Ala Asp Lys
    2165                 2170                 2175

Ile Ser  Gln Ser Glu Thr Tyr  Arg Arg Arg Arg Gln  Glu Trp Glu
    2180                 2185                 2190

Ile Gln  Arg Asn Asn Ala Glu  Ala Glu Leu Lys Gln  Ile Asp Ala
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    2195                2200                2205

Gln Leu  Lys Ser Leu Ala Val  Arg Arg Glu Ala Ala  Val Leu Gln
    2210                2215                2220

Lys Thr  Ser Leu Lys Thr Gln  Gln Glu Gln Thr Gln  Ser Gln Leu
    2225                2230                2235

Ala Phe  Leu Gln Arg Lys Phe  Ser Asn Gln Ala Leu  Tyr Asn Trp
    2240                2245                2250

Leu Arg  Gly Arg Leu Ala Ala  Ile Tyr Phe Gln Phe  Tyr Asp Leu
    2255                2260                2265

Ala Val  Ala Arg Cys Leu Met  Ala Glu Gln Ala Tyr  Arg Trp Glu
    2270                2275                2280

Leu Asn  Asp Asp Ser Ala Arg  Phe Ile Lys Pro Gly  Ala Trp Gln
    2285                2290                2295

Gly Thr  Tyr Ala Gly Leu Leu  Ala Gly Glu Thr Leu  Met Leu Ser
    2300                2305                2310

Leu Ala  Gln Met Glu Asp Ala  His Leu Lys Arg Asp  Lys Arg Ala
    2315                2320                2325

Leu Glu  Val Glu Arg Thr Val  Ser Leu Ala Glu Val  Tyr Ala Gly
    2330                2335                2340

Leu Pro  Lys Asp Asn Gly Pro  Phe Ser Leu Ala Gln  Glu Ile Asp
    2345                2350                2355

Lys Leu  Val Ser Gln Gly Ser  Gly Ser Ala Gly Ser  Gly Asn Asn
    2360                2365                2370

Asn Leu  Ala Phe Gly Ala Gly  Thr Asp Thr Lys Thr  Ser Leu Gln
    2375                2380                2385

Ala Ser  Val Ser Phe Ala Asp  Leu Lys Ile Arg Glu  Asp Tyr Pro
    2390                2395                2400

Ala Ser  Leu Gly Lys Ile Arg  Arg Ile Lys Gln Ile  Ser Val Thr
    2405                2410                2415

Leu Pro  Ala Leu Leu Gly Pro  Tyr Gln Asp Val Gln  Ala Ile Leu
    2420                2425                2430

Ser Tyr  Gly Asp Lys Ala Gly  Leu Ala Asn Gly Cys  Glu Ala Leu
    2435                2440                2445

Ala Val  Ser His Gly Met Asn  Asp Ser Gly Gln Phe  Gln Leu Asp
    2450                2455                2460

Phe Asn  Asp Gly Lys Phe Leu  Pro Phe Glu Gly Ile  Ala Ile Asp
    2465                2470                2475

Gln Gly  Thr Leu Thr Leu Ser  Phe Pro Asn Ala Ser  Met Pro Glu
    2480                2485                2490

Lys Gly  Lys Gln Ala Thr Met  Leu Lys Thr Leu Asn  Asp Ile Ile
    2495                2500                2505

Leu His  Ile Arg Tyr Thr Ile  Lys
    2510                2515


<210> SEQ ID NO 3
<211> LENGTH: 7500
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(7500)

<400> SEQUENCE: 3

atg aac aca ctc aaa tcc gaa tat caa caa gcg tta gga gca ggt ttt       48
Met Asn Thr Leu Lys Ser Glu Tyr Gln Gln Ala Leu Gly Ala Gly Phe
1               5                   10                  15
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aat aat cta acc gat atc tgc cat ctc tct ttt gac gaa ctg cgc aaa       96
Asn Asn Leu Thr Asp Ile Cys His Leu Ser Phe Asp Glu Leu Arg Lys
            20                  25                  30

aaa gtg aag gat aaa ctc tca tgg tca cag acc cag agc tta tat ctt      144
Lys Val Lys Asp Lys Leu Ser Trp Ser Gln Thr Gln Ser Leu Tyr Leu
        35                  40                  45

gaa gca cag cag gtg caa aag gat aac ctt ctg cat gaa gcc cgt att      192
Glu Ala Gln Gln Val Gln Lys Asp Asn Leu Leu His Glu Ala Arg Ile
    50                  55                  60

ctg aaa cgc gca aac cct cat tta caa agt gcg gtc cat ctt gcc ctg      240
Leu Lys Arg Ala Asn Pro His Leu Gln Ser Ala Val His Leu Ala Leu
65                  70                  75                  80

aca gca cct cat gca gac cag caa ggt tat aat agc cga ttt ggc aat      288
Thr Ala Pro His Ala Asp Gln Gln Gly Tyr Asn Ser Arg Phe Gly Asn
                85                  90                  95

cgc gcc agc aaa tat gca gcc cct ggc gca att tcc tcc atg ttt tct      336
Arg Ala Ser Lys Tyr Ala Ala Pro Gly Ala Ile Ser Ser Met Phe Ser
            100                 105                 110

ctt gcg gct tat ctg act gaa ctt tat cgt cag gca cga aat tta cat      384
Leu Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Gln Ala Arg Asn Leu His
        115                 120                 125

gca gaa ggt tcc att tat cat ctg gat acg cgt cgc cca gat cta aaa      432
Ala Glu Gly Ser Ile Tyr His Leu Asp Thr Arg Arg Pro Asp Leu Lys
    130                 135                 140

tca ttg gtg ctc agc cag aaa aat atg aat acg gag att tcc acg ctt      480
Ser Leu Val Leu Ser Gln Lys Asn Met Asn Thr Glu Ile Ser Thr Leu
145                 150                 155                 160

tct ctg tct aat aac atg ttg cta aac agt att aag act cag cct aat      528
Ser Leu Ser Asn Asn Met Leu Leu Asn Ser Ile Lys Thr Gln Pro Asn
                165                 170                 175

ctg aac agc cac gct aaa gtg atg gaa aag tta tca act ttc cgc act      576
Leu Asn Ser His Ala Lys Val Met Glu Lys Leu Ser Thr Phe Arg Thr
            180                 185                 190

tct ggc tca atg cca tat cac gat gct tat gaa agt gta cgt aag att      624
Ser Gly Ser Met Pro Tyr His Asp Ala Tyr Glu Ser Val Arg Lys Ile
        195                 200                 205

att caa tta caa gct cct gtg ttt gaa caa tcc agt aca tta aca gat      672
Ile Gln Leu Gln Ala Pro Val Phe Glu Gln Ser Ser Thr Leu Thr Asp
    210                 215                 220

acg cca atc acc aaa ctg atg tat caa atc tcc ttg ctg ggg att aat      720
Thr Pro Ile Thr Lys Leu Met Tyr Gln Ile Ser Leu Leu Gly Ile Asn
225                 230                 235                 240

gcc tct gtc tca ccg gag ctg ttt act att ctg acg caa aag ata aaa      768
Ala Ser Val Ser Pro Glu Leu Phe Thr Ile Leu Thr Gln Lys Ile Lys
                245                 250                 255

cca gca acc aat gct gat aac act aat gaa cta aaa aaa ctt tat aag      816
Pro Ala Thr Asn Ala Asp Asn Thr Asn Glu Leu Lys Lys Leu Tyr Lys
            260                 265                 270

aag aat ttt ggt gaa att aaa tct att caa atg gca agg gca gaa tac      864
Lys Asn Phe Gly Glu Ile Lys Ser Ile Gln Met Ala Arg Ala Glu Tyr
        275                 280                 285

ctg aaa agt tat tat aat ctg aca gac aaa gaa ctt aac cag ttt agt      912
Leu Lys Ser Tyr Tyr Asn Leu Thr Asp Lys Glu Leu Asn Gln Phe Ser
    290                 295                 300

aaa aag att aaa caa ata gat agc ctg tgg aat ata gga gac gag att      960
Lys Lys Ile Lys Gln Ile Asp Ser Leu Trp Asn Ile Gly Asp Glu Ile
305                 310                 315                 320

acc caa tac cat cta ttg aaa ttc aat aaa gct att aat cta tct cga     1008
Thr Gln Tyr His Leu Leu Lys Phe Asn Lys Ala Ile Asn Leu Ser Arg
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                325                 330                 335

tca acc gag cta tca cca ata atc ctt aac agc att gcc atc gat atc     1056
Ser Thr Glu Leu Ser Pro Ile Ile Leu Asn Ser Ile Ala Ile Asp Ile
            340                 345                 350

ctt aaa aaa aca cct cca gag gat gac tct gac aac cct ttt agg gac     1104
Leu Lys Lys Thr Pro Pro Glu Asp Asp Ser Asp Asn Pro Phe Arg Asp
        355                 360                 365

gac cct gat tac ctt gaa agc ttt caa gac ctt gac ctt agt gac gaa     1152
Asp Pro Asp Tyr Leu Glu Ser Phe Gln Asp Leu Asp Leu Ser Asp Glu
    370                 375                 380

cca gat ata gac gaa gat gta tta aga gaa gct tta cgt gtt aaa gac     1200
Pro Asp Ile Asp Glu Asp Val Leu Arg Glu Ala Leu Arg Val Lys Asp
385                 390                 395                 400

tat atg caa cgt tat ggt att gat gct gag act gca tta ata ctg tgc     1248
Tyr Met Gln Arg Tyr Gly Ile Asp Ala Glu Thr Ala Leu Ile Leu Cys
                405                 410                 415

aaa gca ccc att tca gaa aat cct tct cat ccc gat cta tcc aaa tta     1296
Lys Ala Pro Ile Ser Glu Asn Pro Ser His Pro Asp Leu Ser Lys Leu
            420                 425                 430

cta gca gac atc cat caa tta act att gat gaa tta ggg gta cta ctg     1344
Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Gly Val Leu Leu
        435                 440                 445

gtt gcc ata gat gaa gga aaa acc gat tta tct cag att act cat gac     1392
Val Ala Ile Asp Glu Gly Lys Thr Asp Leu Ser Gln Ile Thr His Asp
    450                 455                 460

aat tta gcg gtt cta att agc aaa ctc tat tcc gtt acc aat tgg ctg     1440
Asn Leu Ala Val Leu Ile Ser Lys Leu Tyr Ser Val Thr Asn Trp Leu
465                 470                 475                 480

cgt aca cgg aaa tgg agt gta tat cag tta ttt gta atg acg acc gat     1488
Arg Thr Arg Lys Trp Ser Val Tyr Gln Leu Phe Val Met Thr Thr Asp
                485                 490                 495

aaa tat aac aaa acc tta acc ccg gaa ata aac aac ctt ctg gat acc     1536
Lys Tyr Asn Lys Thr Leu Thr Pro Glu Ile Asn Asn Leu Leu Asp Thr
            500                 505                 510

gtc tac aat ggc ttg cag aac ttt tac aag gat aat ttg cta aaa ata     1584
Val Tyr Asn Gly Leu Gln Asn Phe Tyr Lys Asp Asn Leu Leu Lys Ile
        515                 520                 525

aaa gat aat cta ttg aaa gcc aaa gaa agt tta cca gaa gac aaa gat     1632
Lys Asp Asn Leu Leu Lys Ala Lys Glu Ser Leu Pro Glu Asp Lys Asp
    530                 535                 540

aat ttg ccg aaa gcc gag caa tat ctg ttg gaa gcc gag aaa tat ctg     1680
Asn Leu Pro Lys Ala Glu Gln Tyr Leu Leu Glu Ala Glu Lys Tyr Leu
545                 550                 555                 560

cta gca gcc gag aaa tat ctg cta gca gcc gag aaa tat cta ttg gaa     1728
Leu Ala Ala Glu Lys Tyr Leu Leu Ala Ala Glu Lys Tyr Leu Leu Glu
                565                 570                 575

gcc aat aaa aat ccg cta gaa gcc aaa aag gct ctg aaa gaa tac gag     1776
Ala Asn Lys Asn Pro Leu Glu Ala Lys Lys Ala Leu Lys Glu Tyr Glu
            580                 585                 590

aaa aat cag gag gca tac gag aaa aat ctg aaa gaa cac gag aaa tat     1824
Lys Asn Gln Glu Ala Tyr Glu Lys Asn Leu Lys Glu His Glu Lys Tyr
        595                 600                 605

ctg ttg aaa gcc gga gaa aat ctg cca gca atc aaa gag aat ttg cta     1872
Leu Leu Lys Ala Gly Glu Asn Leu Pro Ala Ile Lys Glu Asn Leu Leu
    610                 615                 620

aaa atc aag gaa aat ctg cca aaa gcc ata tct cct tat atc gcc gcc     1920
Lys Ile Lys Glu Asn Leu Pro Lys Ala Ile Ser Pro Tyr Ile Ala Ala
625                 630                 635                 640

gct ctg caa ttg cca tct gag aat gtt gct ctc tcc gtg ctg gct tgg     1968
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Ala Leu Gln Leu Pro Ser Glu Asn Val Ala Leu Ser Val Leu Ala Trp
                645                 650                 655

gca gat aaa cta aac tct ggc aaa gaa aac aaa atg acg gca gat tca     2016
Ala Asp Lys Leu Asn Ser Gly Lys Glu Asn Lys Met Thr Ala Asp Ser
            660                 665                 670

ttc tgg aac tgg tta cgg aaa aaa ccc att gaa act caa tcg aaa aca     2064
Phe Trp Asn Trp Leu Arg Lys Lys Pro Ile Glu Thr Gln Ser Lys Thr
        675                 680                 685

act gaa gca act gaa gca act gaa gca act gaa gca act gaa gca act     2112
Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr
    690                 695                 700

gaa gca act gaa aaa act aca cta att caa caa gct gtc caa tat tgc     2160
Glu Ala Thr Glu Lys Thr Thr Leu Ile Gln Gln Ala Val Gln Tyr Cys
705                 710                 715                 720

cag tgc cta gca caa ctg gcg ctg att tat cgc tct acc ggt ctt agc     2208
Gln Cys Leu Ala Gln Leu Ala Leu Ile Tyr Arg Ser Thr Gly Leu Ser
                725                 730                 735

gaa agc act tta cgt ctg ttt gtg aca aat cca caa atc ttt ggt ctt     2256
Glu Ser Thr Leu Arg Leu Phe Val Thr Asn Pro Gln Ile Phe Gly Leu
            740                 745                 750

acc gcg aaa aca acg tca aca cac aat gta tta tca ctg att atg ctg     2304
Thr Ala Lys Thr Thr Ser Thr His Asn Val Leu Ser Leu Ile Met Leu
        755                 760                 765

acg cgt ttt act gac tgg gtt aac tca cta ggt gaa aac gcc tct tct     2352
Thr Arg Phe Thr Asp Trp Val Asn Ser Leu Gly Glu Asn Ala Ser Ser
    770                 775                 780

gta ctg acc gag ttt gaa aaa gga aca tta acg gca gaa cta ttg gct     2400
Val Leu Thr Glu Phe Glu Lys Gly Thr Leu Thr Ala Glu Leu Leu Ala
785                 790                 795                 800

aac gcc atg aat ctt gat aaa aat cta cta gag caa gcc agt act caa     2448
Asn Ala Met Asn Leu Asp Lys Asn Leu Leu Glu Gln Ala Ser Thr Gln
                805                 810                 815

gca caa gct gat ttc tcc aat tgg cca tct atc gac aac cta ttg cag     2496
Ala Gln Ala Asp Phe Ser Asn Trp Pro Ser Ile Asp Asn Leu Leu Gln
            820                 825                 830

tgg att aac atc tcg cgt caa ttg aac atc tcg cca caa ggc gtt tct     2544
Trp Ile Asn Ile Ser Arg Gln Leu Asn Ile Ser Pro Gln Gly Val Ser
        835                 840                 845

gaa ctg gcg aaa ata tta gac ata gaa tct tct act aat tat gcc caa     2592
Glu Leu Ala Lys Ile Leu Asp Ile Glu Ser Ser Thr Asn Tyr Ala Gln
    850                 855                 860

tgg gaa aat gtc gct tca ata tta acc gcc gga cta gat acc caa aaa     2640
Trp Glu Asn Val Ala Ser Ile Leu Thr Ala Gly Leu Asp Thr Gln Lys
865                 870                 875                 880

gcc aat acc cta cat gca ttt ctg ggt gag tct cgc agt act gcg tta     2688
Ala Asn Thr Leu His Ala Phe Leu Gly Glu Ser Arg Ser Thr Ala Leu
                885                 890                 895

agt aca tac tat att tat tct cat aac caa aaa gat cga gaa gaa aga     2736
Ser Thr Tyr Tyr Ile Tyr Ser His Asn Gln Lys Asp Arg Glu Glu Arg
            900                 905                 910

aaa cat acg gta att aaa gac cgt gat gat cta tat caa tac ctg ttg     2784
Lys His Thr Val Ile Lys Asp Arg Asp Asp Leu Tyr Gln Tyr Leu Leu
        915                 920                 925

atc gat aac caa gtc tcc gcc gcc atc aaa acc acg gag att gct gaa     2832
Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr Glu Ile Ala Glu
    930                 935                 940

gct atc gct agt atc caa ctg tat att aac cgc gca ttg aaa aat atg     2880
Ala Ile Ala Ser Ile Gln Leu Tyr Ile Asn Arg Ala Leu Lys Asn Met
945                 950                 955                 960
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gag gga gat acc gac aca agt gtc act agc cgt tta ttc ttc act aac     2928
Glu Gly Asp Thr Asp Thr Ser Val Thr Ser Arg Leu Phe Phe Thr Asn
                965                 970                 975

tgg gat aaa tac aac aaa cgc tac agc acc tgg gct ggt att act aag     2976
Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Gly Ile Thr Lys
            980                 985                 990

ctc ctt tac tac cct gaa aac tat  atc gat ccg aca ctg  cgg atc ggc   3024
Leu Leu Tyr Tyr Pro Glu Asn Tyr  Ile Asp Pro Thr Leu  Arg Ile Gly
        995                 1000                 1005

cag aca  aaa atg atg gat acg  cta ctg caa tcc atc  agc caa agt      3069
Gln Thr  Lys Met Met Asp Thr  Leu Leu Gln Ser Ile  Ser Gln Ser
    1010                 1015                 1020

caa ttg  aat acc gat acc gta  gaa gat gcc ttt aaa  tct tat cta      3114
Gln Leu  Asn Thr Asp Thr Val  Glu Asp Ala Phe Lys  Ser Tyr Leu
    1025                 1030                 1035

acg tca  ttc gaa caa gtg gct  aat ctg gaa gtc atc  agc gcc tat      3159
Thr Ser  Phe Glu Gln Val Ala  Asn Leu Glu Val Ile  Ser Ala Tyr
    1040                 1045                 1050

cat gac  aat att aat aat gac  caa gga ttg acc tat  ttt atc gga      3204
His Asp  Asn Ile Asn Asn Asp  Gln Gly Leu Thr Tyr  Phe Ile Gly
    1055                 1060                 1065

cgc agt  aaa aca gaa gtg aat  caa tat tat tgg cgc  agt gta gat      3249
Arg Ser  Lys Thr Glu Val Asn  Gln Tyr Tyr Trp Arg  Ser Val Asp
    1070                 1075                 1080

cac aat  aaa ttc agc gaa ggt  aaa ttc ccc gct aat  gcc tgg agc      3294
His Asn  Lys Phe Ser Glu Gly  Lys Phe Pro Ala Asn  Ala Trp Ser
    1085                 1090                 1095

gag tgg  cac aaa att gac tgc  cca att aat ccc tac  gaa gat act      3339
Glu Trp  His Lys Ile Asp Cys  Pro Ile Asn Pro Tyr  Glu Asp Thr
    1100                 1105                 1110

atc cgc  ccg gta gtc tac caa  tcc cgc ctg tat att  atc tgg ctg      3384
Ile Arg  Pro Val Val Tyr Gln  Ser Arg Leu Tyr Ile  Ile Trp Leu
    1115                 1120                 1125

gaa cag  aag aag gta act aat  cga gca gaa gga gaa  gct atc aaa      3429
Glu Gln  Lys Lys Val Thr Asn  Arg Ala Glu Gly Glu  Ala Ile Lys
    1130                 1135                 1140

caa gga  agc aaa acg acc aca  agc tat cat tat gaa  ctg aaa ttg      3474
Gln Gly  Ser Lys Thr Thr Thr  Ser Tyr His Tyr Glu  Leu Lys Leu
    1145                 1150                 1155

gca cat  att cgt tat gac ggc  acc tgg aat aca cca  att acc ttt      3519
Ala His  Ile Arg Tyr Asp Gly  Thr Trp Asn Thr Pro  Ile Thr Phe
    1160                 1165                 1170

gat gta  gat gaa aaa ata tct  ggt cta aat tta gaa  ctg aat aaa      3564
Asp Val  Asp Glu Lys Ile Ser  Gly Leu Asn Leu Glu  Leu Asn Lys
    1175                 1180                 1185

gcg tta  ggg ctc tat tgt gca  agt tat caa ggc aaa  gat aaa ttg      3609
Ala Leu  Gly Leu Tyr Cys Ala  Ser Tyr Gln Gly Lys  Asp Lys Leu
    1190                 1195                 1200

ctg gtt  atg ttt tat aaa aaa  cag gag caa tta aat  aat tac aca      3654
Leu Val  Met Phe Tyr Lys Lys  Gln Glu Gln Leu Asn  Asn Tyr Thr
    1205                 1210                 1215

gaa aaa  aca gga aac aca tac  aca gca cca ata aaa  ggg cta tat      3699
Glu Lys  Thr Gly Asn Thr Tyr  Thr Ala Pro Ile Lys  Gly Leu Tyr
    1220                 1225                 1230

atc act  tcc aat atg tct cct  gag gaa atg aca ccc  gaa agt tac      3744
Ile Thr  Ser Asn Met Ser Pro  Glu Glu Met Thr Pro  Glu Ser Tyr
    1235                 1240                 1245

aga ctt  aat gct cat aaa cag  ttt gat acc aac aat  gtc gta aga      3789
Arg Leu  Asn Ala His Lys Gln  Phe Asp Thr Asn Asn  Val Val Arg
    1250                 1255                 1260
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gtc aat  aac cgc tat gca gaa  agc tac gaa atc cct  tca tca gta      3834
Val Asn  Asn Arg Tyr Ala Glu  Ser Tyr Glu Ile Pro  Ser Ser Val
    1265                 1270                 1275

aac agt  aat aat ggt tat gat  tgg gga gag ggc tat  ctg agt atg      3879
Asn Ser  Asn Asn Gly Tyr Asp  Trp Gly Glu Gly Tyr  Leu Ser Met
    1280                 1285                 1290

gta tac  ggc ggg agc att ctg  att acc cgt gac cca  agc gat aac      3924
Val Tyr  Gly Gly Ser Ile Leu  Ile Thr Arg Asp Pro  Ser Asp Asn
    1295                 1300                 1305

tca aaa  atc caa atc tca cca  aag tta aga att att  cat aat gga      3969
Ser Lys  Ile Gln Ile Ser Pro  Lys Leu Arg Ile Ile  His Asn Gly
    1310                 1315                 1320

tat gaa  ggt cga caa cgt aat  caa tgc aat ttg atg  aag aaa tac      4014
Tyr Glu  Gly Arg Gln Arg Asn  Gln Cys Asn Leu Met  Lys Lys Tyr
    1325                 1330                 1335

ggc aag  ctc ggt gat aaa ttc  att att tat act acg  cta ggt att      4059
Gly Lys  Leu Gly Asp Lys Phe  Ile Ile Tyr Thr Thr  Leu Gly Ile
    1340                 1345                 1350

aac ccc  aat aat tta tca aat  aaa aaa ctt atc tac  cct gtt tat      4104
Asn Pro  Asn Asn Leu Ser Asn  Lys Lys Leu Ile Tyr  Pro Val Tyr
    1355                 1360                 1365

caa tat  gaa gga aat gaa agt  aag ctt agt caa gga  aga ctt ctg      4149
Gln Tyr  Glu Gly Asn Glu Ser  Lys Leu Ser Gln Gly  Arg Leu Leu
    1370                 1375                 1380

ttt tat  cgg gat agc acc act  aac ttt aca aga gcc  tgg ttc cct      4194
Phe Tyr  Arg Asp Ser Thr Thr  Asn Phe Thr Arg Ala  Trp Phe Pro
    1385                 1390                 1395

aac ctt  tct tct gac tca aaa  gaa atg tcc ata acc  act ggc ggt      4239
Asn Leu  Ser Ser Asp Ser Lys  Glu Met Ser Ile Thr  Thr Gly Gly
    1400                 1405                 1410

aac att  agt ggt aat tat ggt  tat att gat aac aaa  cat agt gac      4284
Asn Ile  Ser Gly Asn Tyr Gly  Tyr Ile Asp Asn Lys  His Ser Asp
    1415                 1420                 1425

aac aaa  cca ttc gaa gaa tat  ttc tat atg gac gac  cac ggc ggt      4329
Asn Lys  Pro Phe Glu Glu Tyr  Phe Tyr Met Asp Asp  His Gly Gly
    1430                 1435                 1440

att gac  act gac gtt tcg gag  cca ata ttt att aat  aca aaa att      4374
Ile Asp  Thr Asp Val Ser Glu  Pro Ile Phe Ile Asn  Thr Lys Ile
    1445                 1450                 1455

cag cct  tca aat gtt aaa atc  ata gtg aaa aca gtg  aag gat gat      4419
Gln Pro  Ser Asn Val Lys Ile  Ile Val Lys Thr Val  Lys Asp Asp
    1460                 1465                 1470

gga aaa  tta gac agt aaa cca  tat ata gca gaa gac  aaa gtt tca      4464
Gly Lys  Leu Asp Ser Lys Pro  Tyr Ile Ala Glu Asp  Lys Val Ser
    1475                 1480                 1485

gtt aaa  ccg aca cca aac ttt  gaa gaa atg tgt tat  cag ttt aat      4509
Val Lys  Pro Thr Pro Asn Phe  Glu Glu Met Cys Tyr  Gln Phe Asn
    1490                 1495                 1500

aat ctc  gat caa ata gat gtc  tcc act cta gta ttt  aaa aat aat      4554
Asn Leu  Asp Gln Ile Asp Val  Ser Thr Leu Val Phe  Lys Asn Asn
    1505                 1510                 1515

gaa gca  agt att gat atc acc  ttt aca gca tct gct  gac gca ttt      4599
Glu Ala  Ser Ile Asp Ile Thr  Phe Thr Ala Ser Ala  Asp Ala Phe
    1520                 1525                 1530

gaa agt  ggt aaa gaa caa cgt  aat cta ggt gaa gaa  cat ttc agt      4644
Glu Ser  Gly Lys Glu Gln Arg  Asn Leu Gly Glu Glu  His Phe Ser
    1535                 1540                 1545

att cgt  att atc aaa aaa gcg  aat gtt aat gat gtc  ctg acc ctt      4689
Ile Arg  Ile Ile Lys Lys Ala  Asn Val Asn Asp Val  Leu Thr Leu
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    1550                1555                1560

cac cac  gat cca agt ggg gca  caa tat atg caa tgg  gga gcc tat      4734
His His  Asp Pro Ser Gly Ala  Gln Tyr Met Gln Trp  Gly Ala Tyr
    1565                1570                1575

cgt act  cgc ctt aat acc ctg  ttt gcc cgt aaa tta  att agc cgc      4779
Arg Thr  Arg Leu Asn Thr Leu  Phe Ala Arg Lys Leu  Ile Ser Arg
    1580                1585                1590

gcc aat  gcg ggg atc gac act  att ttg agt atg gaa  act cag aat      4824
Ala Asn  Ala Gly Ile Asp Thr  Ile Leu Ser Met Glu  Thr Gln Asn
    1595                1600                1605

att caa  gag cca caa tta ggc  aaa ggc ttt tat gtt  aat ttc act      4869
Ile Gln  Glu Pro Gln Leu Gly  Lys Gly Phe Tyr Val  Asn Phe Thr
    1610                1615                1620

ctt cct  aaa tat gat caa aac  aca cat ggt aat gaa  cgc cag ttt      4914
Leu Pro  Lys Tyr Asp Gln Asn  Thr His Gly Asn Glu  Arg Gln Phe
    1625                1630                1635

aaa att  cat ata ggg aat att  gct ggt gat aat aca  atg cgg cca      4959
Lys Ile  His Ile Gly Asn Ile  Ala Gly Asp Asn Thr  Met Arg Pro
    1640                1645                1650

tat tac  caa gga ata ttg gct  gac acc gaa acc agt  gtc gtt ctt      5004
Tyr Tyr  Gln Gly Ile Leu Ala  Asp Thr Glu Thr Ser  Val Val Leu
    1655                1660                1665

ttt gtc  cct tat gag aaa caa  tct tat acc aat gaa  ggt gtt aga      5049
Phe Val  Pro Tyr Glu Lys Gln  Ser Tyr Thr Asn Glu  Gly Val Arg
    1670                1675                1680

tta gga  gtt gaa tac aaa aaa  gta tct tac cta ggc  gtc tgg gaa      5094
Leu Gly  Val Glu Tyr Lys Lys  Val Ser Tyr Leu Gly  Val Trp Glu
    1685                1690                1695

ccc gct  ttc ttc tat ttc aat  gaa att caa cag aag  ttt att ctg      5139
Pro Ala  Phe Phe Tyr Phe Asn  Glu Ile Gln Gln Lys  Phe Ile Leu
    1700                1705                1710

att aat  gat gcc gat cat aac  tca gca atg act caa  tct ggt gaa      5184
Ile Asn  Asp Ala Asp His Asn  Ser Ala Met Thr Gln  Ser Gly Glu
    1715                1720                1725

aaa aca  gga att aaa aaa tac  aaa ggc ttt ctt gac  gtt tct att      5229
Lys Thr  Gly Ile Lys Lys Tyr  Lys Gly Phe Leu Asp  Val Ser Ile
    1730                1735                1740

ctt atc  gat cat cag cac aca  gaa cca atg gac ttc  aac ggc gcc      5274
Leu Ile  Asp His Gln His Thr  Glu Pro Met Asp Phe  Asn Gly Ala
    1745                1750                1755

aac agc  ctc tac ttc tgg gaa  ctg ttc tac tat acc  ccg atg ctg      5319
Asn Ser  Leu Tyr Phe Trp Glu  Leu Phe Tyr Tyr Thr  Pro Met Leu
    1760                1765                1770

atc gct  caa cgt ttg cta cac  gag caa aat ttc gat  gaa gct aac      5364
Ile Ala  Gln Arg Leu Leu His  Glu Gln Asn Phe Asp  Glu Ala Asn
    1775                1780                1785

cgt tgg  ctg aaa tat gtc tgg  aat cca tct ggt cat  att gcc aat      5409
Arg Trp  Leu Lys Tyr Val Trp  Asn Pro Ser Gly His  Ile Ala Asn
    1790                1795                1800

ggt caa  aaa cag cac ccc cac  aac tgg aat gtc cgc  cca tta caa      5454
Gly Gln  Lys Gln His Pro His  Asn Trp Asn Val Arg  Pro Leu Gln
    1805                1810                1815

gag gac  acc agt tgg aac gat  gat cca ttg gat aca  ttt gat ccc      5499
Glu Asp  Thr Ser Trp Asn Asp  Asp Pro Leu Asp Thr  Phe Asp Pro
    1820                1825                1830

gat gcc  atc gct caa cat gat  ccg atg cac tac aaa  gtc gcc acc      5544
Asp Ala  Ile Ala Gln His Asp  Pro Met His Tyr Lys  Val Ala Thr
    1835                1840                1845

ttt atg  tgc gcc ctt gat cta  ttg atc gaa cag gga  gat tac gcc      5589
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Phe Met  Cys Ala Leu Asp Leu  Leu Ile Glu Gln Gly  Asp Tyr Ala
    1850                 1855                 1860

tat cgc  cag ttg gaa cgg gac  aca ctc gcc gaa gcc  aaa atg tgg      5634
Tyr Arg  Gln Leu Glu Arg Asp  Thr Leu Ala Glu Ala  Lys Met Trp
    1865                 1870                 1875

tat atg  cag gca ctg cat cta  tta ggc gat aaa cct  cat tta tta      5679
Tyr Met  Gln Ala Leu His Leu  Leu Gly Asp Lys Pro  His Leu Leu
    1880                 1885                 1890

ctc agt  tca aca tgg agt gat  cca gag cta aaa gaa  gcc gca gat      5724
Leu Ser  Ser Thr Trp Ser Asp  Pro Glu Leu Lys Glu  Ala Ala Asp
    1895                 1900                 1905

ctt gaa  aaa caa cag gca cat  gcc aaa gca ata gca  gat tta cga      5769
Leu Glu  Lys Gln Gln Ala His  Ala Lys Ala Ile Ala  Asp Leu Arg
    1910                 1915                 1920

caa ggc  cag cct aaa gat gga  agc aac aca gat ctt  ttc ctg cca      5814
Gln Gly  Gln Pro Lys Asp Gly  Ser Asn Thr Asp Leu  Phe Leu Pro
    1925                 1930                 1935

cag gtc  aac gaa gtg atg ttg  agc tat tgg cag aaa  ctg gaa caa      5859
Gln Val  Asn Glu Val Met Leu  Ser Tyr Trp Gln Lys  Leu Glu Gln
    1940                 1945                 1950

cgg tta  tat aac ctg cgc cat  aac ctc tct att gat  ggt caa cct      5904
Arg Leu  Tyr Asn Leu Arg His  Asn Leu Ser Ile Asp  Gly Gln Pro
    1955                 1960                 1965

tta cat  ttg cct att ttc gcg  aca ccg gca gat cca  aaa gcg ctg      5949
Leu His  Leu Pro Ile Phe Ala  Thr Pro Ala Asp Pro  Lys Ala Leu
    1970                 1975                 1980

ctc agc  gcc gct gtc gcc agt  tca caa ggt gga agc  aat ctt ccg      5994
Leu Ser  Ala Ala Val Ala Ser  Ser Gln Gly Gly Ser  Asn Leu Pro
    1985                 1990                 1995

tca gag  ttt ata tca gtt tgg  cgt ttc cca cat atg  ctg gaa aac      6039
Ser Glu  Phe Ile Ser Val Trp  Arg Phe Pro His Met  Leu Glu Asn
    2000                 2005                 2010

gcc cgc  agt atg gtc agt caa  ctc acc caa ttc ggc  tcc aca tta      6084
Ala Arg  Ser Met Val Ser Gln  Leu Thr Gln Phe Gly  Ser Thr Leu
    2015                 2020                 2025

caa aat  att atc gaa cgt cag  gat gcg gaa gca tta  aac acg ctg      6129
Gln Asn  Ile Ile Glu Arg Gln  Asp Ala Glu Ala Leu  Asn Thr Leu
    2030                 2035                 2040

tta cag  aat caa gcg gcg gaa  ctg ata ttg acc aat  ctc agc ata      6174
Leu Gln  Asn Gln Ala Ala Glu  Leu Ile Leu Thr Asn  Leu Ser Ile
    2045                 2050                 2055

cag gac  aaa acc att gaa gag  ctg gat gtt gaa aaa  act gtg cta      6219
Gln Asp  Lys Thr Ile Glu Glu  Leu Asp Val Glu Lys  Thr Val Leu
    2060                 2065                 2070

gaa aaa  acc cgc gcc gga gct  aaa tcg cgt ttt gat  agc tac agc      6264
Glu Lys  Thr Arg Ala Gly Ala  Lys Ser Arg Phe Asp  Ser Tyr Ser
    2075                 2080                 2085

aaa ttc  tac gat gaa gat atc  aac gca ggt gaa aaa  cag gcg atg      6309
Lys Phe  Tyr Asp Glu Asp Ile  Asn Ala Gly Glu Lys  Gln Ala Met
    2090                 2095                 2100

gcg ttg  cga gcc tcc gtc gca  ggc atc tct act gca  ctt caa gca      6354
Ala Leu  Arg Ala Ser Val Ala  Gly Ile Ser Thr Ala  Leu Gln Ala
    2105                 2110                 2115

tca cat  ctg gca ggc gca gcg  ctt gat ttg gct ccc  aac atc ttt      6399
Ser His  Leu Ala Gly Ala Ala  Leu Asp Leu Ala Pro  Asn Ile Phe
    2120                 2125                 2130

ggc ttc  gct gat ggc ggt agc  cat tgg gga gca att  gcc caa gcc      6444
Gly Phe  Ala Asp Gly Gly Ser  His Trp Gly Ala Ile  Ala Gln Ala
    2135                 2140                 2145
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aca agt  aat gtc atg gaa ttc  tcc gcc agt gtc atg  agc acc gaa      6489
Thr Ser  Asn Val Met Glu Phe  Ser Ala Ser Val Met  Ser Thr Glu
    2150                 2155                 2160

gcg gat  aaa atc agc cag tct  gaa gcc tac cgt cgg  cgt cga cag      6534
Ala Asp  Lys Ile Ser Gln Ser  Glu Ala Tyr Arg Arg  Arg Arg Gln
    2165                 2170                 2175

gag tgg  aaa atc cag cgt aac  aac gct gat gca gag  ttg aaa caa      6579
Glu Trp  Lys Ile Gln Arg Asn  Asn Ala Asp Ala Glu  Leu Lys Gln
    2180                 2185                 2190

atc gat  gct caa ctt caa tca  tta gtc gta cgc cgt  gaa gcc gcc      6624
Ile Asp  Ala Gln Leu Gln Ser  Leu Val Val Arg Arg  Glu Ala Ala
    2195                 2200                 2205

gtg ttg  cag aaa acc agc ctg  aaa acc caa caa gag  cag acg cac      6669
Val Leu  Gln Lys Thr Ser Leu  Lys Thr Gln Gln Glu  Gln Thr His
    2210                 2215                 2220

gca caa  ctg acc ttc ctg caa  cat aag ttc agc aat  cag gca tta      6714
Ala Gln  Leu Thr Phe Leu Gln  His Lys Phe Ser Asn  Gln Ala Leu
    2225                 2230                 2235

tac aac  tgg ctg cgt ggt cgg  ctg tcc gcc att tac  ttc cag ttc      6759
Tyr Asn  Trp Leu Arg Gly Arg  Leu Ser Ala Ile Tyr  Phe Gln Phe
    2240                 2245                 2250

tat gat  tta gcg gta gcc cgt  tgc ctg atg gct gaa  atg gcc tat      6804
Tyr Asp  Leu Ala Val Ala Arg  Cys Leu Met Ala Glu  Met Ala Tyr
    2255                 2260                 2265

cgt tgg  gag act aac gat gcc  gca gca cgc ttt atc  aag ccc ggc      6849
Arg Trp  Glu Thr Asn Asp Ala  Ala Ala Arg Phe Ile  Lys Pro Gly
    2270                 2275                 2280

gcc tgg  cag gga acc cat gcc  ggt ctg ctg gcg ggt  gaa acc tta      6894
Ala Trp  Gln Gly Thr His Ala  Gly Leu Leu Ala Gly  Glu Thr Leu
    2285                 2290                 2295

atg ctg  aat cta gca cag atg  gaa gat gcc cac ctg  aaa cag gag      6939
Met Leu  Asn Leu Ala Gln Met  Glu Asp Ala His Leu  Lys Gln Glu
    2300                 2305                 2310

caa cgc  gta ctg gag gta gaa  cgt acc gtt tca cta  gca gaa gtt      6984
Gln Arg  Val Leu Glu Val Glu  Arg Thr Val Ser Leu  Ala Glu Val
    2315                 2320                 2325

tat aaa  gag aaa ggt caa ttt  tct ctg acc aag aaa  att gca gaa      7029
Tyr Lys  Glu Lys Gly Gln Phe  Ser Leu Thr Lys Lys  Ile Ala Glu
    2330                 2335                 2340

ctg gtg  aat aag aaa cca gac  act acc agt agc aga  aat aac aca      7074
Leu Val  Asn Lys Lys Pro Asp  Thr Thr Ser Ser Arg  Asn Asn Thr
    2345                 2350                 2355

ctg aat  ttt ggt gaa gga aat  gcc aaa act tct cta  caa gcg tct      7119
Leu Asn  Phe Gly Glu Gly Asn  Ala Lys Thr Ser Leu  Gln Ala Ser
    2360                 2365                 2370

att tcg  tta gct gac tta caa  att cgt cac gat tac  cca gaa aac      7164
Ile Ser  Leu Ala Asp Leu Gln  Ile Arg His Asp Tyr  Pro Glu Asn
    2375                 2380                 2385

agt gga  gcc ggt aac gtc cgc  cgg att aaa cag atc  agt gtc acc      7209
Ser Gly  Ala Gly Asn Val Arg  Arg Ile Lys Gln Ile  Ser Val Thr
    2390                 2395                 2400

ctg ccg  gca ctg tta gga cct  tat cag gat gtg caa  gcg att ctg      7254
Leu Pro  Ala Leu Leu Gly Pro  Tyr Gln Asp Val Gln  Ala Ile Leu
    2405                 2410                 2415

tct tat  ggc gga gat gcc acc  ggg tta gcc aaa ggt  tgt aaa gcg      7299
Ser Tyr  Gly Gly Asp Ala Thr  Gly Leu Ala Lys Gly  Cys Lys Ala
    2420                 2425                 2430

ctg gca  gtt tct cac gga atg  aat gac agc ggt cag  ttc caa ttg      7344
Leu Ala  Val Ser His Gly Met  Asn Asp Ser Gly Gln  Phe Gln Leu
    2435                 2440                 2445
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gat ttc  aac gat ggc aaa ttc  ctg cca ttt gaa gga  atc gaa atc      7389
Asp Phe  Asn Asp Gly Lys Phe  Leu Pro Phe Glu Gly  Ile Glu Ile
    2450                 2455                 2460

gat aaa  ggt acg ctg aca tta  agc ttc ccg aat gca  acc gaa aaa      7434
Asp Lys  Gly Thr Leu Thr Leu  Ser Phe Pro Asn Ala  Thr Glu Lys
    2465                 2470                 2475

caa aaa  acc atg ctg gag agt  cta agc gac atc att  ctg cat att      7479
Gln Lys  Thr Met Leu Glu Ser  Leu Ser Asp Ile Ile  Leu His Ile
    2480                 2485                 2490

cgc tac  acc att cgc caa taa                                        7500
Arg Tyr  Thr Ile Arg Gln
    2495
```

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<210> SEQ ID NO 4
<211> LENGTH: 2499
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 4

Met Asn Thr Leu Lys Ser Glu Tyr Gln Gln Ala Leu Gly Ala Gly Phe
1               5                   10                  15

Asn Asn Leu Thr Asp Ile Cys His Leu Ser Phe Asp Glu Leu Arg Lys
            20                  25                  30

Lys Val Lys Asp Lys Leu Ser Trp Ser Gln Thr Gln Ser Leu Tyr Leu
        35                  40                  45

Glu Ala Gln Gln Val Gln Lys Asp Asn Leu Leu His Glu Ala Arg Ile
    50                  55                  60

Leu Lys Arg Ala Asn Pro His Leu Gln Ser Ala Val His Leu Ala Leu
65                  70                  75                  80

Thr Ala Pro His Ala Asp Gln Gln Gly Tyr Asn Ser Arg Phe Gly Asn
                85                  90                  95

Arg Ala Ser Lys Tyr Ala Ala Pro Gly Ala Ile Ser Ser Met Phe Ser
            100                 105                 110

Leu Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Gln Ala Arg Asn Leu His
        115                 120                 125

Ala Glu Gly Ser Ile Tyr His Leu Asp Thr Arg Arg Pro Asp Leu Lys
    130                 135                 140

Ser Leu Val Leu Ser Gln Lys Asn Met Asn Thr Glu Ile Ser Thr Leu
145                 150                 155                 160

Ser Leu Ser Asn Asn Met Leu Leu Asn Ser Ile Lys Thr Gln Pro Asn
                165                 170                 175

Leu Asn Ser His Ala Lys Val Met Glu Lys Leu Ser Thr Phe Arg Thr
            180                 185                 190

Ser Gly Ser Met Pro Tyr His Asp Ala Tyr Glu Ser Val Arg Lys Ile
        195                 200                 205

Ile Gln Leu Gln Ala Pro Val Phe Glu Gln Ser Ser Thr Leu Thr Asp
    210                 215                 220

Thr Pro Ile Thr Lys Leu Met Tyr Gln Ile Ser Leu Leu Gly Ile Asn
225                 230                 235                 240

Ala Ser Val Ser Pro Glu Leu Phe Thr Ile Leu Thr Gln Lys Ile Lys
                245                 250                 255

Pro Ala Thr Asn Ala Asp Asn Thr Asn Glu Leu Lys Lys Leu Tyr Lys
            260                 265                 270

Lys Asn Phe Gly Glu Ile Lys Ser Ile Gln Met Ala Arg Ala Glu Tyr
        275                 280                 285
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Leu Lys Ser Tyr Tyr Asn Leu Thr Asp Lys Glu Leu Asn Gln Phe Ser
    290                 295                 300

Lys Lys Ile Lys Gln Ile Asp Ser Leu Trp Asn Ile Gly Asp Glu Ile
305                 310                 315                 320

Thr Gln Tyr His Leu Leu Lys Phe Asn Lys Ala Ile Asn Leu Ser Arg
                325                 330                 335

Ser Thr Glu Leu Ser Pro Ile Ile Leu Asn Ser Ile Ala Ile Asp Ile
            340                 345                 350

Leu Lys Lys Thr Pro Pro Glu Asp Asp Ser Asp Asn Pro Phe Arg Asp
        355                 360                 365

Asp Pro Asp Tyr Leu Glu Ser Phe Gln Asp Leu Asp Leu Ser Asp Glu
    370                 375                 380

Pro Asp Ile Asp Glu Asp Val Leu Arg Glu Ala Leu Arg Val Lys Asp
385                 390                 395                 400

Tyr Met Gln Arg Tyr Gly Ile Asp Ala Glu Thr Ala Leu Ile Leu Cys
                405                 410                 415

Lys Ala Pro Ile Ser Glu Asn Pro Ser His Pro Asp Leu Ser Lys Leu
            420                 425                 430

Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Gly Val Leu Leu
        435                 440                 445

Val Ala Ile Asp Glu Gly Lys Thr Asp Leu Ser Gln Ile Thr His Asp
    450                 455                 460

Asn Leu Ala Val Leu Ile Ser Lys Leu Tyr Ser Val Thr Asn Trp Leu
465                 470                 475                 480

Arg Thr Arg Lys Trp Ser Val Tyr Gln Leu Phe Val Met Thr Thr Asp
                485                 490                 495

Lys Tyr Asn Lys Thr Leu Thr Pro Glu Ile Asn Asn Leu Leu Asp Thr
            500                 505                 510

Val Tyr Asn Gly Leu Gln Asn Phe Tyr Lys Asp Asn Leu Leu Lys Ile
        515                 520                 525

Lys Asp Asn Leu Leu Lys Ala Lys Glu Ser Leu Pro Glu Asp Lys Asp
    530                 535                 540

Asn Leu Pro Lys Ala Glu Gln Tyr Leu Leu Glu Ala Glu Lys Tyr Leu
545                 550                 555                 560

Leu Ala Ala Glu Lys Tyr Leu Leu Ala Ala Glu Lys Tyr Leu Leu Glu
                565                 570                 575

Ala Asn Lys Asn Pro Leu Glu Ala Lys Lys Ala Leu Lys Glu Tyr Glu
            580                 585                 590

Lys Asn Gln Glu Ala Tyr Glu Lys Asn Leu Lys Glu His Glu Lys Tyr
        595                 600                 605

Leu Leu Lys Ala Gly Glu Asn Leu Pro Ala Ile Lys Glu Asn Leu Leu
    610                 615                 620

Lys Ile Lys Glu Asn Leu Pro Lys Ala Ile Ser Pro Tyr Ile Ala Ala
625                 630                 635                 640

Ala Leu Gln Leu Pro Ser Glu Asn Val Ala Leu Ser Val Leu Ala Trp
                645                 650                 655

Ala Asp Lys Leu Asn Ser Gly Lys Glu Asn Lys Met Thr Ala Asp Ser
            660                 665                 670

Phe Trp Asn Trp Leu Arg Lys Lys Pro Ile Glu Thr Gln Ser Lys Thr
        675                 680                 685

Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr Glu Ala Thr
    690                 695                 700

Glu Ala Thr Glu Lys Thr Thr Leu Ile Gln Gln Ala Val Gln Tyr Cys
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705                 710                 715                 720

Gln Cys Leu Ala Gln Leu Ala Leu Ile Tyr Arg Ser Thr Gly Leu Ser
                725                 730                 735

Glu Ser Thr Leu Arg Leu Phe Val Thr Asn Pro Gln Ile Phe Gly Leu
            740                 745                 750

Thr Ala Lys Thr Thr Ser Thr His Asn Val Leu Ser Leu Ile Met Leu
        755                 760                 765

Thr Arg Phe Thr Asp Trp Val Asn Ser Leu Gly Glu Asn Ala Ser Ser
    770                 775                 780

Val Leu Thr Glu Phe Glu Lys Gly Thr Leu Thr Ala Glu Leu Leu Ala
785                 790                 795                 800

Asn Ala Met Asn Leu Asp Lys Asn Leu Leu Glu Gln Ala Ser Thr Gln
                805                 810                 815

Ala Gln Ala Asp Phe Ser Asn Trp Pro Ser Ile Asp Asn Leu Leu Gln
            820                 825                 830

Trp Ile Asn Ile Ser Arg Gln Leu Asn Ile Ser Pro Gln Gly Val Ser
        835                 840                 845

Glu Leu Ala Lys Ile Leu Asp Ile Glu Ser Ser Thr Asn Tyr Ala Gln
    850                 855                 860

Trp Glu Asn Val Ala Ser Ile Leu Thr Ala Gly Leu Asp Thr Gln Lys
865                 870                 875                 880

Ala Asn Thr Leu His Ala Phe Leu Gly Glu Ser Arg Ser Thr Ala Leu
                885                 890                 895

Ser Thr Tyr Tyr Ile Tyr Ser His Asn Gln Lys Asp Arg Glu Glu Arg
            900                 905                 910

Lys His Thr Val Ile Lys Asp Arg Asp Asp Leu Tyr Gln Tyr Leu Leu
        915                 920                 925

Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr Glu Ile Ala Glu
    930                 935                 940

Ala Ile Ala Ser Ile Gln Leu Tyr Ile Asn Arg Ala Leu Lys Asn Met
945                 950                 955                 960

Glu Gly Asp Thr Asp Thr Ser Val Thr Ser Arg Leu Phe Phe Thr Asn
                965                 970                 975

Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Gly Ile Thr Lys
            980                 985                 990

Leu Leu Tyr Tyr Pro Glu Asn Tyr  Ile Asp Pro Thr Leu  Arg Ile Gly
        995                 1000                1005

Gln Thr  Lys Met Met Asp Thr  Leu Leu Gln Ser Ile  Ser Gln Ser
    1010                 1015                 1020

Gln Leu  Asn Thr Asp Thr Val  Glu Asp Ala Phe Lys  Ser Tyr Leu
    1025                 1030                 1035

Thr Ser  Phe Glu Gln Val Ala  Asn Leu Glu Val Ile  Ser Ala Tyr
    1040                 1045                 1050

His Asp  Asn Ile Asn Asn Asp  Gln Gly Leu Thr Tyr  Phe Ile Gly
    1055                 1060                 1065

Arg Ser  Lys Thr Glu Val Asn  Gln Tyr Tyr Trp Arg  Ser Val Asp
    1070                 1075                 1080

His Asn  Lys Phe Ser Glu Gly  Lys Phe Pro Ala Asn  Ala Trp Ser
    1085                 1090                 1095

Glu Trp  His Lys Ile Asp Cys  Pro Ile Asn Pro Tyr  Glu Asp Thr
    1100                 1105                 1110

Ile Arg  Pro Val Val Tyr Gln  Ser Arg Leu Tyr Ile  Ile Trp Leu
    1115                 1120                 1125
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Glu Gln  Lys Lys Val Thr Asn  Arg Ala Glu Gly Glu  Ala Ile Lys
    1130                 1135                 1140

Gln Gly  Ser Lys Thr Thr Thr  Ser Tyr His Tyr Glu  Leu Lys Leu
    1145                 1150                 1155

Ala His  Ile Arg Tyr Asp Gly  Thr Trp Asn Thr Pro  Ile Thr Phe
    1160                 1165                 1170

Asp Val  Asp Glu Lys Ile Ser  Gly Leu Asn Leu Glu  Leu Asn Lys
    1175                 1180                 1185

Ala Leu  Gly Leu Tyr Cys Ala  Ser Tyr Gln Gly Lys  Asp Lys Leu
    1190                 1195                 1200

Leu Val  Met Phe Tyr Lys Lys  Gln Glu Gln Leu Asn  Asn Tyr Thr
    1205                 1210                 1215

Glu Lys  Thr Gly Asn Thr Tyr  Thr Ala Pro Ile Lys  Gly Leu Tyr
    1220                 1225                 1230

Ile Thr  Ser Asn Met Ser Pro  Glu Glu Met Thr Pro  Glu Ser Tyr
    1235                 1240                 1245

Arg Leu  Asn Ala His Lys Gln  Phe Asp Thr Asn Asn  Val Val Arg
    1250                 1255                 1260

Val Asn  Asn Arg Tyr Ala Glu  Ser Tyr Glu Ile Pro  Ser Ser Val
    1265                 1270                 1275

Asn Ser  Asn Asn Gly Tyr Asp  Trp Gly Glu Gly Tyr  Leu Ser Met
    1280                 1285                 1290

Val Tyr  Gly Gly Ser Ile Leu  Ile Thr Arg Asp Pro  Ser Asp Asn
    1295                 1300                 1305

Ser Lys  Ile Gln Ile Ser Pro  Lys Leu Arg Ile Ile  His Asn Gly
    1310                 1315                 1320

Tyr Glu  Gly Arg Gln Arg Asn  Gln Cys Asn Leu Met  Lys Lys Tyr
    1325                 1330                 1335

Gly Lys  Leu Gly Asp Lys Phe  Ile Ile Tyr Thr Thr  Leu Gly Ile
    1340                 1345                 1350

Asn Pro  Asn Asn Leu Ser Asn  Lys Lys Leu Ile Tyr  Pro Val Tyr
    1355                 1360                 1365

Gln Tyr  Glu Gly Asn Glu Ser  Lys Leu Ser Gln Gly  Arg Leu Leu
    1370                 1375                 1380

Phe Tyr  Arg Asp Ser Thr Thr  Asn Phe Thr Arg Ala  Trp Phe Pro
    1385                 1390                 1395

Asn Leu  Ser Ser Asp Ser Lys  Glu Met Ser Ile Thr  Thr Gly Gly
    1400                 1405                 1410

Asn Ile  Ser Gly Asn Tyr Gly  Tyr Ile Asp Asn Lys  His Ser Asp
    1415                 1420                 1425

Asn Lys  Pro Phe Glu Glu Tyr  Phe Tyr Met Asp Asp  His Gly Gly
    1430                 1435                 1440

Ile Asp  Thr Asp Val Ser Glu  Pro Ile Phe Ile Asn  Thr Lys Ile
    1445                 1450                 1455

Gln Pro  Ser Asn Val Lys Ile  Ile Val Lys Thr Val  Lys Asp Asp
    1460                 1465                 1470

Gly Lys  Leu Asp Ser Lys Pro  Tyr Ile Ala Glu Asp  Lys Val Ser
    1475                 1480                 1485

Val Lys  Pro Thr Pro Asn Phe  Glu Glu Met Cys Tyr  Gln Phe Asn
    1490                 1495                 1500

Asn Leu  Asp Gln Ile Asp Val  Ser Thr Leu Val Phe  Lys Asn Asn
    1505                 1510                 1515
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Glu Ala  Ser Ile Asp Ile Thr  Phe Thr Ala Ser Ala  Asp Ala Phe
    1520                 1525                 1530

Glu Ser  Gly Lys Glu Gln Arg  Asn Leu Gly Glu Glu  His Phe Ser
    1535                 1540                 1545

Ile Arg  Ile Ile Lys Lys Ala  Asn Val Asn Asp Val  Leu Thr Leu
    1550                 1555                 1560

His His  Asp Pro Ser Gly Ala  Gln Tyr Met Gln Trp  Gly Ala Tyr
    1565                 1570                 1575

Arg Thr  Arg Leu Asn Thr Leu  Phe Ala Arg Lys Leu  Ile Ser Arg
    1580                 1585                 1590

Ala Asn  Ala Gly Ile Asp Thr  Ile Leu Ser Met Glu  Thr Gln Asn
    1595                 1600                 1605

Ile Gln  Glu Pro Gln Leu Gly  Lys Gly Phe Tyr Val  Asn Phe Thr
    1610                 1615                 1620

Leu Pro  Lys Tyr Asp Gln Asn  Thr His Gly Asn Glu  Arg Gln Phe
    1625                 1630                 1635

Lys Ile  His Ile Gly Asn Ile  Ala Gly Asp Asn Thr  Met Arg Pro
    1640                 1645                 1650

Tyr Tyr  Gln Gly Ile Leu Ala  Asp Thr Glu Thr Ser  Val Val Leu
    1655                 1660                 1665

Phe Val  Pro Tyr Glu Lys Gln  Ser Tyr Thr Asn Glu  Gly Val Arg
    1670                 1675                 1680

Leu Gly  Val Glu Tyr Lys Lys  Val Ser Tyr Leu Gly  Val Trp Glu
    1685                 1690                 1695

Pro Ala  Phe Phe Tyr Phe Asn  Glu Ile Gln Gln Lys  Phe Ile Leu
    1700                 1705                 1710

Ile Asn  Asp Ala Asp His Asn  Ser Ala Met Thr Gln  Ser Gly Glu
    1715                 1720                 1725

Lys Thr  Gly Ile Lys Lys Tyr  Lys Gly Phe Leu Asp  Val Ser Ile
    1730                 1735                 1740

Leu Ile  Asp His Gln His Thr  Glu Pro Met Asp Phe  Asn Gly Ala
    1745                 1750                 1755

Asn Ser  Leu Tyr Phe Trp Glu  Leu Phe Tyr Tyr Thr  Pro Met Leu
    1760                 1765                 1770

Ile Ala  Gln Arg Leu Leu His  Glu Gln Asn Phe Asp  Glu Ala Asn
    1775                 1780                 1785

Arg Trp  Leu Lys Tyr Val Trp  Asn Pro Ser Gly His  Ile Ala Asn
    1790                 1795                 1800

Gly Gln  Lys Gln His Pro His  Asn Trp Asn Val Arg  Pro Leu Gln
    1805                 1810                 1815

Glu Asp  Thr Ser Trp Asn Asp  Asp Pro Leu Asp Thr  Phe Asp Pro
    1820                 1825                 1830

Asp Ala  Ile Ala Gln His Asp  Pro Met His Tyr Lys  Val Ala Thr
    1835                 1840                 1845

Phe Met  Cys Ala Leu Asp Leu  Leu Ile Glu Gln Gly  Asp Tyr Ala
    1850                 1855                 1860

Tyr Arg  Gln Leu Glu Arg Asp  Thr Leu Ala Glu Ala  Lys Met Trp
    1865                 1870                 1875

Tyr Met  Gln Ala Leu His Leu  Leu Gly Asp Lys Pro  His Leu Leu
    1880                 1885                 1890

Leu Ser  Ser Thr Trp Ser Asp  Pro Glu Leu Lys Glu  Ala Ala Asp
    1895                 1900                 1905

Leu Glu  Lys Gln Gln Ala His  Ala Lys Ala Ile Ala  Asp Leu Arg
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    1910                1915                1920

Gln Gly  Gln Pro Lys Asp Gly  Ser Asn Thr Asp Leu  Phe Leu Pro
    1925                1930                1935

Gln Val  Asn Glu Val Met Leu  Ser Tyr Trp Gln Lys  Leu Glu Gln
    1940                1945                1950

Arg Leu  Tyr Asn Leu Arg His  Asn Leu Ser Ile Asp  Gly Gln Pro
    1955                1960                1965

Leu His  Leu Pro Ile Phe Ala  Thr Pro Ala Asp Pro  Lys Ala Leu
    1970                1975                1980

Leu Ser  Ala Ala Val Ala Ser  Ser Gln Gly Gly Ser  Asn Leu Pro
    1985                1990                1995

Ser Glu  Phe Ile Ser Val Trp  Arg Phe Pro His Met  Leu Glu Asn
    2000                2005                2010

Ala Arg  Ser Met Val Ser Gln  Leu Thr Gln Phe Gly  Ser Thr Leu
    2015                2020                2025

Gln Asn  Ile Ile Glu Arg Gln  Asp Ala Glu Ala Leu  Asn Thr Leu
    2030                2035                2040

Leu Gln  Asn Gln Ala Ala Glu  Leu Ile Leu Thr Asn  Leu Ser Ile
    2045                2050                2055

Gln Asp  Lys Thr Ile Glu Glu  Leu Asp Val Glu Lys  Thr Val Leu
    2060                2065                2070

Glu Lys  Thr Arg Ala Gly Ala  Lys Ser Arg Phe Asp  Ser Tyr Ser
    2075                2080                2085

Lys Phe  Tyr Asp Glu Asp Ile  Asn Ala Gly Glu Lys  Gln Ala Met
    2090                2095                2100

Ala Leu  Arg Ala Ser Val Ala  Gly Ile Ser Thr Ala  Leu Gln Ala
    2105                2110                2115

Ser His  Leu Ala Gly Ala Ala  Leu Asp Leu Ala Pro  Asn Ile Phe
    2120                2125                2130

Gly Phe  Ala Asp Gly Gly Ser  His Trp Gly Ala Ile  Ala Gln Ala
    2135                2140                2145

Thr Ser  Asn Val Met Glu Phe  Ser Ala Ser Val Met  Ser Thr Glu
    2150                2155                2160

Ala Asp  Lys Ile Ser Gln Ser  Glu Ala Tyr Arg Arg  Arg Arg Gln
    2165                2170                2175

Glu Trp  Lys Ile Gln Arg Asn  Asn Ala Asp Ala Glu  Leu Lys Gln
    2180                2185                2190

Ile Asp  Ala Gln Leu Gln Ser  Leu Val Val Arg Arg  Glu Ala Ala
    2195                2200                2205

Val Leu  Gln Lys Thr Ser Leu  Lys Thr Gln Gln Glu  Gln Thr His
    2210                2215                2220

Ala Gln  Leu Thr Phe Leu Gln  His Lys Phe Ser Asn  Gln Ala Leu
    2225                2230                2235

Tyr Asn  Trp Leu Arg Gly Arg  Leu Ser Ala Ile Tyr  Phe Gln Phe
    2240                2245                2250

Tyr Asp  Leu Ala Val Ala Arg  Cys Leu Met Ala Glu  Met Ala Tyr
    2255                2260                2265

Arg Trp  Glu Thr Asn Asp Ala  Ala Ala Arg Phe Ile  Lys Pro Gly
    2270                2275                2280

Ala Trp  Gln Gly Thr His Ala  Gly Leu Leu Ala Gly  Glu Thr Leu
    2285                2290                2295

Met Leu  Asn Leu Ala Gln Met  Glu Asp Ala His Leu  Lys Gln Glu
    2300                2305                2310
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Gln Arg  Val Leu Glu Val Glu  Arg Thr Val Ser Leu  Ala Glu Val
    2315                2320                2325

Tyr Lys  Glu Lys Gly Gln Phe  Ser Leu Thr Lys Lys  Ile Ala Glu
    2330                2335                2340

Leu Val  Asn Lys Lys Pro Asp  Thr Thr Ser Ser Arg  Asn Asn Thr
    2345                2350                2355

Leu Asn  Phe Gly Glu Gly Asn  Ala Lys Thr Ser Leu  Gln Ala Ser
    2360                2365                2370

Ile Ser  Leu Ala Asp Leu Gln  Ile Arg His Asp Tyr  Pro Glu Asn
    2375                2380                2385

Ser Gly  Ala Gly Asn Val Arg  Arg Ile Lys Gln Ile  Ser Val Thr
    2390                2395                2400

Leu Pro  Ala Leu Leu Gly Pro  Tyr Gln Asp Val Gln  Ala Ile Leu
    2405                2410                2415

Ser Tyr  Gly Gly Asp Ala Thr  Gly Leu Ala Lys Gly  Cys Lys Ala
    2420                2425                2430

Leu Ala  Val Ser His Gly Met  Asn Asp Ser Gly Gln  Phe Gln Leu
    2435                2440                2445

Asp Phe  Asn Asp Gly Lys Phe  Leu Pro Phe Glu Gly  Ile Glu Ile
    2450                2455                2460

Asp Lys  Gly Thr Leu Thr Leu  Ser Phe Pro Asn Ala  Thr Glu Lys
    2465                2470                2475

Gln Lys  Thr Met Leu Glu Ser  Leu Ser Asp Ile Ile  Leu His Ile
    2480                2485                2490

Arg Tyr  Thr Ile Arg Gln
    2495


<210> SEQ ID NO 5
<211> LENGTH: 6534
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
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atg agc aca atc acg cca gaa cac cct gaa atg gca caa cag gca caa         48
Met Ser Thr Ile Thr Pro Glu His Pro Glu Met Ala Gln Gln Ala Gln
1               5                   10                  15

aaa gca aac cga ctg cat gag gcg agt atc ctc aaa cgt gct aac ccc         96
Lys Ala Asn Arg Leu His Glu Ala Ser Ile Leu Lys Arg Ala Asn Pro
            20                  25                  30

caa tta caa aat gcg gta cat ctt gct tta acc aca ccc cat gct gac        144
Gln Leu Gln Asn Ala Val His Leu Ala Leu Thr Thr Pro His Ala Asp
        35                  40                  45

cag caa ggt tat aac agt aaa ttt ggt ggc cgc gcc agc cag tat gtc        192
Gln Gln Gly Tyr Asn Ser Lys Phe Gly Gly Arg Ala Ser Gln Tyr Val
    50                  55                  60

gct ccc ggc gca gtt gct tcc atg ttc tct ccc gcc gct tat ctg acc        240
Ala Pro Gly Ala Val Ala Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
65                  70                  75                  80

gaa ctt tat cgt cag gca cag gat tta cat aaa aaa gag tcc att tat        288
Glu Leu Tyr Arg Gln Ala Gln Asp Leu His Lys Lys Glu Ser Ile Tyr
                85                  90                  95

cat ctg gat aaa cgc cgc cct gat tta aaa tca ctg aca ctc agc cag        336
His Leu Asp Lys Arg Arg Pro Asp Leu Lys Ser Leu Thr Leu Ser Gln
            100                 105                 110
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caa aat atg gat gat gaa gtt tct aca ctt tct cta tct aat aag gtg       384
Gln Asn Met Asp Asp Glu Val Ser Thr Leu Ser Leu Ser Asn Lys Val
        115                 120                 125

ttg ctg gaa ggg atc aag acg ctg acc ggg ctg gaa ggc cat act aac       432
Leu Leu Glu Gly Ile Lys Thr Leu Thr Gly Leu Glu Gly His Thr Asn
    130                 135                 140

gtg atg aaa gcg cta tca acc ttt cgc tct tct ggc tct ctg cca tat       480
Val Met Lys Ala Leu Ser Thr Phe Arg Ser Ser Gly Ser Leu Pro Tyr
145                 150                 155                 160

cac gat gct tac gaa agt gta cgt aag gtt att caa tta caa gct ccg       528
His Asp Ala Tyr Glu Ser Val Arg Lys Val Ile Gln Leu Gln Ala Pro
                165                 170                 175

ata ttc gac caa gtt ggt cca tcc cca gaa aca gat atc gcc aat ctg       576
Ile Phe Asp Gln Val Gly Pro Ser Pro Glu Thr Asp Ile Ala Asn Leu
            180                 185                 190

aca tat caa gct tcc ctg ctg gga att aat gct tct gtc ttg cct gaa       624
Thr Tyr Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Val Leu Pro Glu
        195                 200                 205

ttg ttt aag act ctg aca gaa gag atc acc gaa gtt aat gca aat gag       672
Leu Phe Lys Thr Leu Thr Glu Glu Ile Thr Glu Val Asn Ala Asn Glu
    210                 215                 220

aag ttt aag aaa aac ttt ggg gat aga gag cca tca gaa ctt ctc act       720
Lys Phe Lys Lys Asn Phe Gly Asp Arg Glu Pro Ser Glu Leu Leu Thr
225                 230                 235                 240

ctg gat gcc ttg aaa cac tat tac aat tta acc aat gaa gaa tta gaa       768
Leu Asp Ala Leu Lys His Tyr Tyr Asn Leu Thr Asn Glu Glu Leu Glu
                245                 250                 255

cag ttt tta aat cac gta tta ata gaa agt aac tct act tac aca aat       816
Gln Phe Leu Asn His Val Leu Ile Glu Ser Asn Ser Thr Tyr Thr Asn
            260                 265                 270

aac caa ctt att aat ata agc att gat aca tca ggt aag ata caa ttg       864
Asn Gln Leu Ile Asn Ile Ser Ile Asp Thr Ser Gly Lys Ile Gln Leu
        275                 280                 285

agc cgc ata aca cga aca cct gac tta aat tat aac aac ctc aat tac       912
Ser Arg Ile Thr Arg Thr Pro Asp Leu Asn Tyr Asn Asn Leu Asn Tyr
    290                 295                 300

atg aat tta tat cct att caa aac aga cgt ttt tat gtt gat att agc       960
Met Asn Leu Tyr Pro Ile Gln Asn Arg Arg Phe Tyr Val Asp Ile Ser
305                 310                 315                 320

tat aag aaa aaa gct ggg caa gtt agt att aga ctc agc aag ccc cag      1008
Tyr Lys Lys Lys Ala Gly Gln Val Ser Ile Arg Leu Ser Lys Pro Gln
                325                 330                 335

tct aaa tat ctc aaa ggt ata tat aaa gcg acc ata gaa aac acg aac      1056
Ser Lys Tyr Leu Lys Gly Ile Tyr Lys Ala Thr Ile Glu Asn Thr Asn
            340                 345                 350

tat tct tcc cca aca ttt gaa tta acc gac aaa gat att caa aaa gaa      1104
Tyr Ser Ser Pro Thr Phe Glu Leu Thr Asp Lys Asp Ile Gln Lys Glu
        355                 360                 365

ttt act ctt cta agt tat cgt tat aaa gaa aat agt gat tcg aat ata      1152
Phe Thr Leu Leu Ser Tyr Arg Tyr Lys Glu Asn Ser Asp Ser Asn Ile
    370                 375                 380

tct gac tca tct tat gcc aag ttc aaa att cag gat tat tca cct gca      1200
Ser Asp Ser Ser Tyr Ala Lys Phe Lys Ile Gln Asp Tyr Ser Pro Ala
385                 390                 395                 400

att ttt ctg tta aaa ctt aat aaa acc att cgt ttg tcc cac gca aca      1248
Ile Phe Leu Leu Lys Leu Asn Lys Thr Ile Arg Leu Ser His Ala Thr
                405                 410                 415

aaa ctt ctg cca aca gta ctg gaa aaa att gtc ttc aat atc aat cag      1296
Lys Leu Leu Pro Thr Val Leu Glu Lys Ile Val Phe Asn Ile Asn Gln
            420                 425                 430
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aaa cta gat atc aat gca gaa ata tta aag aaa ata ttt cgc gtt aaa     1344
Lys Leu Asp Ile Asn Ala Glu Ile Leu Lys Lys Ile Phe Arg Val Lys
        435                 440                 445

tac tat atg caa cgt tac ggt att gat gct gag act gca ttg gta ctg     1392
Tyr Tyr Met Gln Arg Tyr Gly Ile Asp Ala Glu Thr Ala Leu Val Leu
    450                 455                 460

tgc aaa gta tca act aat ata att aat cct tct agt tcc gat cta atc     1440
Cys Lys Val Ser Thr Asn Ile Ile Asn Pro Ser Ser Ser Asp Leu Ile
465                 470                 475                 480

aaa tta cta gca aat att cat cag tta act gtt aat gag ctg aat tta     1488
Lys Leu Leu Ala Asn Ile His Gln Leu Thr Val Asn Glu Leu Asn Leu
                485                 490                 495

ctg ctg gtt gcc ata ggt gaa gga tca acc aat cta tct gag ctc agt     1536
Leu Leu Val Ala Ile Gly Glu Gly Ser Thr Asn Leu Ser Glu Leu Ser
            500                 505                 510

gat aac aat cta tct gtt ctg att gat aaa ctt tat agc att acc cag     1584
Asp Asn Asn Leu Ser Val Leu Ile Asp Lys Leu Tyr Ser Ile Thr Gln
        515                 520                 525

tgg ttg cgt aca cgg aaa tgg aat atg tac ctg ctg ttt atg atg act     1632
Trp Leu Arg Thr Arg Lys Trp Asn Met Tyr Leu Leu Phe Met Met Thr
    530                 535                 540

acc acc gac tat aac caa acc ctg acg ccg gaa att cag aac ctg cta     1680
Thr Thr Asp Tyr Asn Gln Thr Leu Thr Pro Glu Ile Gln Asn Leu Leu
545                 550                 555                 560

gat gct gtt tac aat ggt ttg caa aac ttt aac agt aaa aac gaa gca     1728
Asp Ala Val Tyr Asn Gly Leu Gln Asn Phe Asn Ser Lys Asn Glu Ala
                565                 570                 575

aat ctt ctg ttg aag atc tcg cct tac atc gcc gcc gct ctg caa ttg     1776
Asn Leu Leu Leu Lys Ile Ser Pro Tyr Ile Ala Ala Ala Leu Gln Leu
            580                 585                 590

ccg tct gaa aat acc gct tat tat ata ctc aac tgg gca gat caa cta     1824
Pro Ser Glu Asn Thr Ala Tyr Tyr Ile Leu Asn Trp Ala Asp Gln Leu
        595                 600                 605

aaa cct ggc tct ggt gca atg aca gca aca aaa ttc tgg gaa tgg ttg     1872
Lys Pro Gly Ser Gly Ala Met Thr Ala Thr Lys Phe Trp Glu Trp Leu
    610                 615                 620

caa gct tca cat aat cca gag caa tca acc gct ata aca gaa gaa caa     1920
Gln Ala Ser His Asn Pro Glu Gln Ser Thr Ala Ile Thr Glu Glu Gln
625                 630                 635                 640

gca gtc caa tat tgc caa tgc ctg gca caa ttg gca ctg att tat cgt     1968
Ala Val Gln Tyr Cys Gln Cys Leu Ala Gln Leu Ala Leu Ile Tyr Arg
                645                 650                 655

tcc acc ggc ctt agc gaa agc act tta cgt ctg ttt gtc aca aaa cca     2016
Ser Thr Gly Leu Ser Glu Ser Thr Leu Arg Leu Phe Val Thr Lys Pro
            660                 665                 670

caa ctc ttt ggc ttt acc gaa gga aca gcg tca aca cac aat gca tta     2064
Gln Leu Phe Gly Phe Thr Glu Gly Thr Ala Ser Thr His Asn Ala Leu
        675                 680                 685

tca ctg ata aag ctg aca cgt ttt act gac tgg gtt aac tct ctg ggt     2112
Ser Leu Ile Lys Leu Thr Arg Phe Thr Asp Trp Val Asn Ser Leu Gly
    690                 695                 700

gaa aaa gcc tct tct gta ctg acc gaa ttt gag aag gga aca tta aca     2160
Glu Lys Ala Ser Ser Val Leu Thr Glu Phe Glu Lys Gly Thr Leu Thr
705                 710                 715                 720

gca gaa cta ttg gct aac gcc ctg agt ctt gat aaa aat cta ctg gag     2208
Ala Glu Leu Leu Ala Asn Ala Leu Ser Leu Asp Lys Asn Leu Leu Glu
                725                 730                 735

caa gcc agt aat caa gca caa gtt aat ttc acc gac tgg ccg tct atc     2256
Gln Ala Ser Asn Gln Ala Gln Val Asn Phe Thr Asp Trp Pro Ser Ile
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            740                 745                 750

gat acc atc cag caa tgg att aac att gcg cgt caa ttg aat atc tct         2304
Asp Thr Ile Gln Gln Trp Ile Asn Ile Ala Arg Gln Leu Asn Ile Ser
        755                 760                 765

cca caa gac gtt tct gca cta gcg caa gta ctc acc aca gaa tcc tcc         2352
Pro Gln Asp Val Ser Ala Leu Ala Gln Val Leu Thr Thr Glu Ser Ser
    770                 775                 780

gat aac tat gcc gaa tgg gaa aac gtc gcg gcg aca tta acc gcc gga         2400
Asp Asn Tyr Ala Glu Trp Glu Asn Val Ala Ala Thr Leu Thr Ala Gly
785                 790                 795                 800

ctg gac acc caa aaa gcc aac gcc ctg cac acc ttt ctg gat gaa tct         2448
Leu Asp Thr Gln Lys Ala Asn Ala Leu His Thr Phe Leu Asp Glu Ser
                805                 810                 815

cgt agt gct gca tta agc gag tac tat atc cgt aaa gtc gct aac gca         2496
Arg Ser Ala Ala Leu Ser Glu Tyr Tyr Ile Arg Lys Val Ala Asn Ala
            820                 825                 830

ggt gca aaa gtt aaa aac cat gat gat ctg tac cag tat tta ttg att         2544
Gly Ala Lys Val Lys Asn His Asp Asp Leu Tyr Gln Tyr Leu Leu Ile
        835                 840                 845

gat aac caa gtt tcc gcc gcc atc aaa acc acc ccg att gca gaa gct         2592
Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr Pro Ile Ala Glu Ala
    850                 855                 860

atc gcc agc atc caa ctg tat att aac cgg gca ctg aaa aat atg gag         2640
Ile Ala Ser Ile Gln Leu Tyr Ile Asn Arg Ala Leu Lys Asn Met Glu
865                 870                 875                 880

gaa aac gcg gtt tcg cag gtc gtc act cga cca ttc ttt acc gat tgg         2688
Glu Asn Ala Val Ser Gln Val Val Thr Arg Pro Phe Phe Thr Asp Trp
                885                 890                 895

gac aaa tac aat aaa cgc tac agc acc tgg gcc agc att gct aaa ctc         2736
Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Ser Ile Ala Lys Leu
            900                 905                 910

att tac tac cct gag aat tac atc gat ccg aca ata cgc atc ggg cga         2784
Ile Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr Ile Arg Ile Gly Arg
        915                 920                 925

aca aaa atg atg gat aca ttg ctg caa tcc atc agc cag agt caa tta         2832
Thr Lys Met Met Asp Thr Leu Leu Gln Ser Ile Ser Gln Ser Gln Leu
    930                 935                 940

aat acc gat acg gta gaa gac gcc ttt atg tct tat ctg acg tcg ttc         2880
Asn Thr Asp Thr Val Glu Asp Ala Phe Met Ser Tyr Leu Thr Ser Phe
945                 950                 955                 960

gaa cag ata gct aat ctg gaa gtc gtc agc gcc tat cat gac aat gcc         2928
Glu Gln Ile Ala Asn Leu Glu Val Val Ser Ala Tyr His Asp Asn Ala
                965                 970                 975

aaa gat gat caa aga tta acc tat ttt atc ggg cac agt aaa acc gaa         2976
Lys Asp Asp Gln Arg Leu Thr Tyr Phe Ile Gly His Ser Lys Thr Glu
            980                 985                 990

gtt aat caa tat tac tgg cgt aac  gtg gat cac aat aaa  ttc agc gac   3024
Val Asn Gln Tyr Tyr Trp Arg Asn  Val Asp His Asn Lys  Phe Ser Asp
        995                 1000                 1005

gat aaa  ttc cct gcc aat gcc  tgg agt gag tgg cac  aaa att gat      3069
Asp Lys  Phe Pro Ala Asn Ala  Trp Ser Glu Trp His  Lys Ile Asp
    1010                 1015                 1020

tgt cca  ata aat ccc tat cag  ggc act atc cat ccg  gta att ttc      3114
Cys Pro  Ile Asn Pro Tyr Gln  Gly Thr Ile His Pro  Val Ile Phe
    1025                 1030                 1035

caa tcc  cga ctg tat ctg atc  tgg ttg gag cag aag  aaa att gct      3159
Gln Ser  Arg Leu Tyr Leu Ile  Trp Leu Glu Gln Lys  Lys Ile Ala
    1040                 1045                 1050

aaa cag  gca gat aat aat caa  acc gtt gaa gat tat  tat tat gaa      3204
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Lys Gln  Ala Asp Asn Asn Gln  Thr Val Glu Asp Tyr  Tyr Tyr Glu
    1055                1060                1065

cta aaa  cta gca cat atc cgt  tat gac ggt act tgg  aat aca cca      3249
Leu Lys  Leu Ala His Ile Arg  Tyr Asp Gly Thr Trp  Asn Thr Pro
    1070                1075                1080

gta gcc  ttt aat atc aat gac  aaa gta tct gct gtt  tta aaa atg      3294
Val Ala  Phe Asn Ile Asn Asp  Lys Val Ser Ala Val  Leu Lys Met
    1085                1090                1095

tca aat  cca cca gca act tcg  gaa tta tta gag tca  cca gag tca      3339
Ser Asn  Pro Pro Ala Thr Ser  Glu Leu Leu Glu Ser  Pro Glu Ser
    1100                1105                1110

tta aaa  cta gga ttc tat tgt  aca aat cat caa gac  aat aaa ttg      3384
Leu Lys  Leu Gly Phe Tyr Cys  Thr Asn His Gln Asp  Asn Lys Leu
    1115                1120                1125

ctg gta  atg ttt tat cgc aaa  cga gat gaa ctg gat  gaa tat aag      3429
Leu Val  Met Phe Tyr Arg Lys  Arg Asp Glu Leu Asp  Glu Tyr Lys
    1130                1135                1140

aga aca  tta aaa gag tta gca  gaa gca gaa aaa aag  gta aaa gaa      3474
Arg Thr  Leu Lys Glu Leu Ala  Glu Ala Glu Lys Lys  Val Lys Glu
    1145                1150                1155

ata gca  aaa aaa att gat cgc  gaa gat gga ata tca  gta tct gat      3519
Ile Ala  Lys Lys Ile Asp Arg  Glu Asp Gly Ile Ser  Val Ser Asp
    1160                1165                1170

cat caa  gaa aaa caa aca gca  gaa aag aaa tta aaa  gaa tta ata      3564
His Gln  Glu Lys Gln Thr Ala  Glu Lys Lys Leu Lys  Glu Leu Ile
    1175                1180                1185

caa gag  tta atg caa gga gtg  tat atc tcc tcc aat  atg tta ttg      3609
Gln Glu  Leu Met Gln Gly Val  Tyr Ile Ser Ser Asn  Met Leu Leu
    1190                1195                1200

gaa aat  ata gaa tct gaa cag  tac aaa aat att tat  gaa ctc acc      3654
Glu Asn  Ile Glu Ser Glu Gln  Tyr Lys Asn Ile Tyr  Glu Leu Thr
    1205                1210                1215

tat agt  aaa ttt gat att aac  aat atc ata aag gtg  aat agc tgg      3699
Tyr Ser  Lys Phe Asp Ile Asn  Asn Ile Ile Lys Val  Asn Ser Trp
    1220                1225                1230

aat cct  gtt acc gat gag gtt  aac gac gat aat atc  ctg act gtt      3744
Asn Pro  Val Thr Asp Glu Val  Asn Asp Asp Asn Ile  Leu Thr Val
    1235                1240                1245

cac aat  gat aca aac ggg gcg  caa tat atg cag tcg  gga ggt tat      3789
His Asn  Asp Thr Asn Gly Ala  Gln Tyr Met Gln Ser  Gly Gly Tyr
    1250                1255                1260

cgt act  cgc ctt aat acg ctg  ttt gcc cgt aaa tta  att agt cgc      3834
Arg Thr  Arg Leu Asn Thr Leu  Phe Ala Arg Lys Leu  Ile Ser Arg
    1265                1270                1275

gcc acg  gcc gga ata gat act  att tta aat ata gag  acg cag aaa      3879
Ala Thr  Ala Gly Ile Asp Thr  Ile Leu Asn Ile Glu  Thr Gln Lys
    1280                1285                1290

ctg cca  gaa cct cag tta ggg  aaa gga ttt ttt act  aat ctc att      3924
Leu Pro  Glu Pro Gln Leu Gly  Lys Gly Phe Phe Thr  Asn Leu Ile
    1295                1300                1305

ctt cct  aaa tat gac caa aat  gta cat ggc agc gaa  cgt tgg ttt      3969
Leu Pro  Lys Tyr Asp Gln Asn  Val His Gly Ser Glu  Arg Trp Phe
    1310                1315                1320

aaa att  cat ata aga aat gat  aat aaa atg atg aac  tta tac cac      4014
Lys Ile  His Ile Arg Asn Asp  Asn Lys Met Met Asn  Leu Tyr His
    1325                1330                1335

aaa gga  aca cta act gat act  gaa act agc gtc act  ctt ttt atc      4059
Lys Gly  Thr Leu Thr Asp Thr  Glu Thr Ser Val Thr  Leu Phe Ile
    1340                1345                1350
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cct tgg  tct aat aca caa gaa  cgc gtc gaa ata gca  gta gaa tat      4104
Pro Trp  Ser Asn Thr Gln Glu  Arg Val Glu Ile Ala  Val Glu Tyr
    1355                 1360                 1365

aat aag  aag ttc tat aag gat  caa caa aac tgg gaa  act gct tta      4149
Asn Lys  Lys Phe Tyr Lys Asp  Gln Gln Asn Trp Glu  Thr Ala Leu
    1370                 1375                 1380

ttt cat  ttt aat gaa act aat  cag aaa ttt atg ttg  gtt aat gat      4194
Phe His  Phe Asn Glu Thr Asn  Gln Lys Phe Met Leu  Val Asn Asp
    1385                 1390                 1395

gct gat  aat aag caa gta gta  ata aac gat act gat  gca atc gtc      4239
Ala Asp  Asn Lys Gln Val Val  Ile Asn Asp Thr Asp  Ala Ile Val
    1400                 1405                 1410

aat aaa  tat aaa ggc ttt ctt  gat gtt tcc att ctt  atc gat cag      4284
Asn Lys  Tyr Lys Gly Phe Leu  Asp Val Ser Ile Leu  Ile Asp Gln
    1415                 1420                 1425

cac acg  gaa cca atg gat ttc  agc ggt gct aac agc  ctc tat ttt      4329
His Thr  Glu Pro Met Asp Phe  Ser Gly Ala Asn Ser  Leu Tyr Phe
    1430                 1435                 1440

tgg gaa  cta ttc tac tat gcc  cca atg ctg att gct  cag cgc ctg      4374
Trp Glu  Leu Phe Tyr Tyr Ala  Pro Met Leu Ile Ala  Gln Arg Leu
    1445                 1450                 1455

cta cac  gaa caa cac ttc gat  gaa gcc aac cgt tgg  ttg aaa tat      4419
Leu His  Glu Gln His Phe Asp  Glu Ala Asn Arg Trp  Leu Lys Tyr
    1460                 1465                 1470

atc tgg  aat cca tct ggt tat  att gag cat ggt cag  att cag cac      4464
Ile Trp  Asn Pro Ser Gly Tyr  Ile Glu His Gly Gln  Ile Gln His
    1475                 1480                 1485

tac cgc  tgg aat gtc cgc cca  tta ttg gaa gat atc  agt tgg aac      4509
Tyr Arg  Trp Asn Val Arg Pro  Leu Leu Glu Asp Ile  Ser Trp Asn
    1490                 1495                 1500

gat gat  cca ctg aat tca gtc  gat ccc gat gcc ata  gca caa tat      4554
Asp Asp  Pro Leu Asn Ser Val  Asp Pro Asp Ala Ile  Ala Gln Tyr
    1505                 1510                 1515

gat cca  atg cac tat aaa gtc  gtt act ttt atg cgc  acc ctt gat      4599
Asp Pro  Met His Tyr Lys Val  Val Thr Phe Met Arg  Thr Leu Asp
    1520                 1525                 1530

ctg ttg  ctg gac cgt gga gat  tac gcc tat cgt cag  tta gaa cgg      4644
Leu Leu  Leu Asp Arg Gly Asp  Tyr Ala Tyr Arg Gln  Leu Glu Arg
    1535                 1540                 1545

gac acg  ctt aat gaa gct aag  atg tgg tat atg caa  gca ctg cat      4689
Asp Thr  Leu Asn Glu Ala Lys  Met Trp Tyr Met Gln  Ala Leu His
    1550                 1555                 1560

ctg tta  ggc gat aaa cct cat  cta tct ttc agt tca  acg tgg cgt      4734
Leu Leu  Gly Asp Lys Pro His  Leu Ser Phe Ser Ser  Thr Trp Arg
    1565                 1570                 1575

aaa ccg  agt tta ggt gac gct  gcc aga acg gaa aaa  cag gag gaa      4779
Lys Pro  Ser Leu Gly Asp Ala  Ala Arg Thr Glu Lys  Gln Glu Glu
    1580                 1585                 1590

caa gcc  cat gca atg act gcc  ctg cga caa ggt gat  att agt cgg      4824
Gln Ala  His Ala Met Thr Ala  Leu Arg Gln Gly Asp  Ile Ser Arg
    1595                 1600                 1605

cac aac  cac ccg aca gat ctt  ttc ttg cca cag gtc  aat gaa gtg      4869
His Asn  His Pro Thr Asp Leu  Phe Leu Pro Gln Val  Asn Glu Val
    1610                 1615                 1620

atg caa  aac tac tgg cag aaa  ctg gag caa cgg ctg  tac aac ctg      4914
Met Gln  Asn Tyr Trp Gln Lys  Leu Glu Gln Arg Leu  Tyr Asn Leu
    1625                 1630                 1635

cgc cat  aat ctc tct atc gac  ggc caa ctg cta cat  ctg cct att      4959
Arg His  Asn Leu Ser Ile Asp  Gly Gln Leu Leu His  Leu Pro Ile
    1640                 1645                 1650
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tac gct  aca ccg gca gat cca  aaa gcg tta ctc agt  gcc gct gtt      5004
Tyr Ala  Thr Pro Ala Asp Pro  Lys Ala Leu Leu Ser  Ala Ala Val
    1655                 1660                 1665

gcc aac  tca caa ggc gga agc  aag tta cca atg tca  ttt atg tca      5049
Ala Asn  Ser Gln Gly Gly Ser  Lys Leu Pro Met Ser  Phe Met Ser
    1670                 1675                 1680

ctg tgg  cgt ttc cca cag atg  ttg gaa aac gcg cgc  ggt atg gta      5094
Leu Trp  Arg Phe Pro Gln Met  Leu Glu Asn Ala Arg  Gly Met Val
    1685                 1690                 1695

agc cag  tta aca cag ttc ggc  tcc acg tta caa aat  att atc gaa      5139
Ser Gln  Leu Thr Gln Phe Gly  Ser Thr Leu Gln Asn  Ile Ile Glu
    1700                 1705                 1710

cgt cag  gat gcg gaa gcc tta  aac acg cta ttg cag  aat caa gcg      5184
Arg Gln  Asp Ala Glu Ala Leu  Asn Thr Leu Leu Gln  Asn Gln Ala
    1715                 1720                 1725

gca gaa  ctg ata ttg act aat  ctc agc ata cag gac  aaa acc ctg      5229
Ala Glu  Leu Ile Leu Thr Asn  Leu Ser Ile Gln Asp  Lys Thr Leu
    1730                 1735                 1740

gaa gag  ctg gat gcg gaa aaa  atc gta ctg gag aaa  tcc aaa gct      5274
Glu Glu  Leu Asp Ala Glu Lys  Ile Val Leu Glu Lys  Ser Lys Ala
    1745                 1750                 1755

gga gcg  caa tca cgc ttt aac  agc tac aaa aag cta  tac gat gaa      5319
Gly Ala  Gln Ser Arg Phe Asn  Ser Tyr Lys Lys Leu  Tyr Asp Glu
    1760                 1765                 1770

aat atc  aat gcg ggt gaa aac  cgg gta ata gca ttg  cat tcc tcc      5364
Asn Ile  Asn Ala Gly Glu Asn  Arg Val Ile Ala Leu  His Ser Ser
    1775                 1780                 1785

gtt gct  ggc ctt agc act gcc  ctg caa gca tcg cgt  ctg gca ggc      5409
Val Ala  Gly Leu Ser Thr Ala  Leu Gln Ala Ser Arg  Leu Ala Gly
    1790                 1795                 1800

gcc gcc  ctt gat ctg gcg ccc  aac att ttc ggc ttc  gct gat ggc      5454
Ala Ala  Leu Asp Leu Ala Pro  Asn Ile Phe Gly Phe  Ala Asp Gly
    1805                 1810                 1815

ggc agc  cgt tgg ggg gca att  gcc gaa gcg aca ggt  aat gtc atg      5499
Gly Ser  Arg Trp Gly Ala Ile  Ala Glu Ala Thr Gly  Asn Val Met
    1820                 1825                 1830

gaa ttc  tcc gca aat gtt atg  aac acc gaa gcg gat  aaa atc agc      5544
Glu Phe  Ser Ala Asn Val Met  Asn Thr Glu Ala Asp  Lys Ile Ser
    1835                 1840                 1845

cag tct  gaa acc tat cgc cgt  cgc cgt cag gag tgg  gaa atc caa      5589
Gln Ser  Glu Thr Tyr Arg Arg  Arg Arg Gln Glu Trp  Glu Ile Gln
    1850                 1855                 1860

cgt aac  aat gcc gaa gca gag  ata aaa caa atc gat  gcc caa ctt      5634
Arg Asn  Asn Ala Glu Ala Glu  Ile Lys Gln Ile Asp  Ala Gln Leu
    1865                 1870                 1875

caa tcg  ttg gca gta cgc cgt  gaa gct gcg gtg ttg  cag aaa acc      5679
Gln Ser  Leu Ala Val Arg Arg  Glu Ala Ala Val Leu  Gln Lys Thr
    1880                 1885                 1890

agc ctg  aaa acc caa cag gaa  cag act cag gcg caa  ttg act ttc      5724
Ser Leu  Lys Thr Gln Gln Glu  Gln Thr Gln Ala Gln  Leu Thr Phe
    1895                 1900                 1905

cta caa  cgt aaa ttc agt aat  caa gcg ttg tac cac  tgg cta cgt      5769
Leu Gln  Arg Lys Phe Ser Asn  Gln Ala Leu Tyr His  Trp Leu Arg
    1910                 1915                 1920

ggt cgg  cta gct gct atc tac  ttc caa ttt tac gat  ttg gcc gta      5814
Gly Arg  Leu Ala Ala Ile Tyr  Phe Gln Phe Tyr Asp  Leu Ala Val
    1925                 1930                 1935

acc cgt  tgt ctg atg gca gaa  atg gct tat cgt tgg  gag act cat      5859
Thr Arg  Cys Leu Met Ala Glu  Met Ala Tyr Arg Trp  Glu Thr His
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    1940                1945                1950

aat acc  aca gca agc ttt atc  aaa ccc ggc gcc tgg  cag ggg acg      5904
Asn Thr  Thr Ala Ser Phe Ile  Lys Pro Gly Ala Trp  Gln Gly Thr
    1955                1960                1965

cac gct  ggt ctg ctc gcc ggt  gaa acc ttg atg ctg  aat ctg gca      5949
His Ala  Gly Leu Leu Ala Gly  Glu Thr Leu Met Leu  Asn Leu Ala
    1970                1975                1980

caa atg  gag gat gct tat ttg  aga tgg gat caa cgc  gct ctg gaa      5994
Gln Met  Glu Asp Ala Tyr Leu  Arg Trp Asp Gln Arg  Ala Leu Glu
    1985                1990                1995

gtg gaa  cgt act att tca ctg  gcg caa ctc tat gga  aca cta cca      6039
Val Glu  Arg Thr Ile Ser Leu  Ala Gln Leu Tyr Gly  Thr Leu Pro
    2000                2005                2010

gaa aaa  tca ttt aat ttg gca  aca cgt att tct gcc  cta cta aca      6084
Glu Lys  Ser Phe Asn Leu Ala  Thr Arg Ile Ser Ala  Leu Leu Thr
    2015                2020                2025

ggt agt  aca act gaa ccc gtt  gag gag cat ccc gtt  aca tta gaa      6129
Gly Ser  Thr Thr Glu Pro Val  Glu Glu His Pro Val  Thr Leu Glu
    2030                2035                2040

aac ggt  caa cta agc gcc aaa  atc tct ctg tca ggt  ctg tca cta      6174
Asn Gly  Gln Leu Ser Ala Lys  Ile Ser Leu Ser Gly  Leu Ser Leu
    2045                2050                2055

cat aat  gac tac cca gaa ggc  aat ggc gta ggc aac  att cgg cgc      6219
His Asn  Asp Tyr Pro Glu Gly  Asn Gly Val Gly Asn  Ile Arg Arg
    2060                2065                2070

att aaa  cag atc agt gtc acc  ctg cca gct ctg tta  ggg cca tac      6264
Ile Lys  Gln Ile Ser Val Thr  Leu Pro Ala Leu Leu  Gly Pro Tyr
    2075                2080                2085

caa aat  gta caa gcc att ttg  gcc tac gag gga agt  gaa atc gga      6309
Gln Asn  Val Gln Ala Ile Leu  Ala Tyr Glu Gly Ser  Glu Ile Gly
    2090                2095                2100

tta gct  gag agc tgt aaa tca  ctg gca att tct cat  ggg gtt aat      6354
Leu Ala  Glu Ser Cys Lys Ser  Leu Ala Ile Ser His  Gly Val Asn
    2105                2110                2115

gac agt  ggt caa ttc cag ttg  gat ttc aac aat ggt  aaa ttc ctg      6399
Asp Ser  Gly Gln Phe Gln Leu  Asp Phe Asn Asn Gly  Lys Phe Leu
    2120                2125                2130

ccg ttt  gaa ggg ata gcg att  aac gat acc ggc aca  tta aca ctc      6444
Pro Phe  Glu Gly Ile Ala Ile  Asn Asp Thr Gly Thr  Leu Thr Leu
    2135                2140                2145

aat ttc  ccg aat gcg acc ggc  aaa cag caa gcc atg  tta caa gca      6489
Asn Phe  Pro Asn Ala Thr Gly  Lys Gln Gln Ala Met  Leu Gln Ala
    2150                2155                2160

ttg agc  gat att att ctg cat  att cgc tac acc atc  cgc caa taa      6534
Leu Ser  Asp Ile Ile Leu His  Ile Arg Tyr Thr Ile  Arg Gln
    2165                2170                2175


<210> SEQ ID NO 6
<211> LENGTH: 2177
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 6

Met Ser Thr Ile Thr Pro Glu His Pro Glu Met Ala Gln Gln Ala Gln
1               5                   10                  15

Lys Ala Asn Arg Leu His Glu Ala Ser Ile Leu Lys Arg Ala Asn Pro
            20                  25                  30

Gln Leu Gln Asn Ala Val His Leu Ala Leu Thr Thr Pro His Ala Asp
        35                  40                  45
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Gln Gln Gly Tyr Asn Ser Lys Phe Gly Gly Arg Ala Ser Gln Tyr Val
    50                  55                  60

Ala Pro Gly Ala Val Ala Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
65                  70                  75                  80

Glu Leu Tyr Arg Gln Ala Gln Asp Leu His Lys Lys Glu Ser Ile Tyr
                85                  90                  95

His Leu Asp Lys Arg Arg Pro Asp Leu Lys Ser Leu Thr Leu Ser Gln
            100                 105                 110

Gln Asn Met Asp Asp Glu Val Ser Thr Leu Ser Leu Ser Asn Lys Val
        115                 120                 125

Leu Leu Glu Gly Ile Lys Thr Leu Thr Gly Leu Glu Gly His Thr Asn
    130                 135                 140

Val Met Lys Ala Leu Ser Thr Phe Arg Ser Ser Gly Ser Leu Pro Tyr
145                 150                 155                 160

His Asp Ala Tyr Glu Ser Val Arg Lys Val Ile Gln Leu Gln Ala Pro
                165                 170                 175

Ile Phe Asp Gln Val Gly Pro Ser Pro Glu Thr Asp Ile Ala Asn Leu
            180                 185                 190

Thr Tyr Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Val Leu Pro Glu
        195                 200                 205

Leu Phe Lys Thr Leu Thr Glu Glu Ile Thr Glu Val Asn Ala Asn Glu
    210                 215                 220

Lys Phe Lys Lys Asn Phe Gly Asp Arg Glu Pro Ser Glu Leu Leu Thr
225                 230                 235                 240

Leu Asp Ala Leu Lys His Tyr Tyr Asn Leu Thr Asn Glu Glu Leu Glu
                245                 250                 255

Gln Phe Leu Asn His Val Leu Ile Glu Ser Asn Ser Thr Tyr Thr Asn
            260                 265                 270

Asn Gln Leu Ile Asn Ile Ser Ile Asp Thr Ser Gly Lys Ile Gln Leu
        275                 280                 285

Ser Arg Ile Thr Arg Thr Pro Asp Leu Asn Tyr Asn Asn Leu Asn Tyr
    290                 295                 300

Met Asn Leu Tyr Pro Ile Gln Asn Arg Arg Phe Tyr Val Asp Ile Ser
305                 310                 315                 320

Tyr Lys Lys Lys Ala Gly Gln Val Ser Ile Arg Leu Ser Lys Pro Gln
                325                 330                 335

Ser Lys Tyr Leu Lys Gly Ile Tyr Lys Ala Thr Ile Glu Asn Thr Asn
            340                 345                 350

Tyr Ser Ser Pro Thr Phe Glu Leu Thr Asp Lys Asp Ile Gln Lys Glu
        355                 360                 365

Phe Thr Leu Leu Ser Tyr Arg Tyr Lys Glu Asn Ser Asp Ser Asn Ile
    370                 375                 380

Ser Asp Ser Ser Tyr Ala Lys Phe Lys Ile Gln Asp Tyr Ser Pro Ala
385                 390                 395                 400

Ile Phe Leu Leu Lys Leu Asn Lys Thr Ile Arg Leu Ser His Ala Thr
                405                 410                 415

Lys Leu Leu Pro Thr Val Leu Glu Lys Ile Val Phe Asn Ile Asn Gln
            420                 425                 430

Lys Leu Asp Ile Asn Ala Glu Ile Leu Lys Lys Ile Phe Arg Val Lys
        435                 440                 445

Tyr Tyr Met Gln Arg Tyr Gly Ile Asp Ala Glu Thr Ala Leu Val Leu
    450                 455                 460

Cys Lys Val Ser Thr Asn Ile Ile Asn Pro Ser Ser Ser Asp Leu Ile
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465                 470                 475                 480

Lys Leu Leu Ala Asn Ile His Gln Leu Thr Val Asn Glu Leu Asn Leu
                485                 490                 495

Leu Leu Val Ala Ile Gly Glu Gly Ser Thr Asn Leu Ser Glu Leu Ser
            500                 505                 510

Asp Asn Asn Leu Ser Val Leu Ile Asp Lys Leu Tyr Ser Ile Thr Gln
        515                 520                 525

Trp Leu Arg Thr Arg Lys Trp Asn Met Tyr Leu Leu Phe Met Met Thr
    530                 535                 540

Thr Thr Asp Tyr Asn Gln Thr Leu Thr Pro Glu Ile Gln Asn Leu Leu
545                 550                 555                 560

Asp Ala Val Tyr Asn Gly Leu Gln Asn Phe Asn Ser Lys Asn Glu Ala
                565                 570                 575

Asn Leu Leu Leu Lys Ile Ser Pro Tyr Ile Ala Ala Ala Leu Gln Leu
            580                 585                 590

Pro Ser Glu Asn Thr Ala Tyr Tyr Ile Leu Asn Trp Ala Asp Gln Leu
        595                 600                 605

Lys Pro Gly Ser Gly Ala Met Thr Ala Thr Lys Phe Trp Glu Trp Leu
    610                 615                 620

Gln Ala Ser His Asn Pro Glu Gln Ser Thr Ala Ile Thr Glu Glu Gln
625                 630                 635                 640

Ala Val Gln Tyr Cys Gln Cys Leu Ala Gln Leu Ala Leu Ile Tyr Arg
                645                 650                 655

Ser Thr Gly Leu Ser Glu Ser Thr Leu Arg Leu Phe Val Thr Lys Pro
            660                 665                 670

Gln Leu Phe Gly Phe Thr Glu Gly Thr Ala Ser Thr His Asn Ala Leu
        675                 680                 685

Ser Leu Ile Lys Leu Thr Arg Phe Thr Asp Trp Val Asn Ser Leu Gly
    690                 695                 700

Glu Lys Ala Ser Ser Val Leu Thr Glu Phe Glu Lys Gly Thr Leu Thr
705                 710                 715                 720

Ala Glu Leu Leu Ala Asn Ala Leu Ser Leu Asp Lys Asn Leu Leu Glu
                725                 730                 735

Gln Ala Ser Asn Gln Ala Gln Val Asn Phe Thr Asp Trp Pro Ser Ile
            740                 745                 750

Asp Thr Ile Gln Gln Trp Ile Asn Ile Ala Arg Gln Leu Asn Ile Ser
        755                 760                 765

Pro Gln Asp Val Ser Ala Leu Ala Gln Val Leu Thr Thr Glu Ser Ser
    770                 775                 780

Asp Asn Tyr Ala Glu Trp Glu Asn Val Ala Ala Thr Leu Thr Ala Gly
785                 790                 795                 800

Leu Asp Thr Gln Lys Ala Asn Ala Leu His Thr Phe Leu Asp Glu Ser
                805                 810                 815

Arg Ser Ala Ala Leu Ser Glu Tyr Tyr Ile Arg Lys Val Ala Asn Ala
            820                 825                 830

Gly Ala Lys Val Lys Asn His Asp Asp Leu Tyr Gln Tyr Leu Leu Ile
        835                 840                 845

Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr Pro Ile Ala Glu Ala
    850                 855                 860

Ile Ala Ser Ile Gln Leu Tyr Ile Asn Arg Ala Leu Lys Asn Met Glu
865                 870                 875                 880

Glu Asn Ala Val Ser Gln Val Val Thr Arg Pro Phe Phe Thr Asp Trp
                885                 890                 895
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Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Ser Ile Ala Lys Leu
            900                 905                 910

Ile Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr Ile Arg Ile Gly Arg
        915                 920                 925

Thr Lys Met Met Asp Thr Leu Leu Gln Ser Ile Ser Gln Ser Gln Leu
    930                 935                 940

Asn Thr Asp Thr Val Glu Asp Ala Phe Met Ser Tyr Leu Thr Ser Phe
945                 950                 955                 960

Glu Gln Ile Ala Asn Leu Glu Val Val Ser Ala Tyr His Asp Asn Ala
                965                 970                 975

Lys Asp Asp Gln Arg Leu Thr Tyr Phe Ile Gly His Ser Lys Thr Glu
            980                 985                 990

Val Asn Gln Tyr Tyr Trp Arg Asn  Val Asp His Asn Lys  Phe Ser Asp
        995                 1000                 1005

Asp Lys  Phe Pro Ala Asn Ala  Trp Ser Glu Trp His  Lys Ile Asp
    1010                 1015                 1020

Cys Pro  Ile Asn Pro Tyr Gln  Gly Thr Ile His Pro  Val Ile Phe
    1025                 1030                 1035

Gln Ser  Arg Leu Tyr Leu Ile  Trp Leu Glu Gln Lys  Lys Ile Ala
    1040                 1045                 1050

Lys Gln  Ala Asp Asn Asn Gln  Thr Val Glu Asp Tyr  Tyr Tyr Glu
    1055                 1060                 1065

Leu Lys  Leu Ala His Ile Arg  Tyr Asp Gly Thr Trp  Asn Thr Pro
    1070                 1075                 1080

Val Ala  Phe Asn Ile Asn Asp  Lys Val Ser Ala Val  Leu Lys Met
    1085                 1090                 1095

Ser Asn  Pro Pro Ala Thr Ser  Glu Leu Leu Glu Ser  Pro Glu Ser
    1100                 1105                 1110

Leu Lys  Leu Gly Phe Tyr Cys  Thr Asn His Gln Asp  Asn Lys Leu
    1115                 1120                 1125

Leu Val  Met Phe Tyr Arg Lys  Arg Asp Glu Leu Asp  Glu Tyr Lys
    1130                 1135                 1140

Arg Thr  Leu Lys Glu Leu Ala  Glu Ala Glu Lys Lys  Val Lys Glu
    1145                 1150                 1155

Ile Ala  Lys Lys Ile Asp Arg  Glu Asp Gly Ile Ser  Val Ser Asp
    1160                 1165                 1170

His Gln  Glu Lys Gln Thr Ala  Glu Lys Lys Leu Lys  Glu Leu Ile
    1175                 1180                 1185

Gln Glu  Leu Met Gln Gly Val  Tyr Ile Ser Ser Asn  Met Leu Leu
    1190                 1195                 1200

Glu Asn  Ile Glu Ser Glu Gln  Tyr Lys Asn Ile Tyr  Glu Leu Thr
    1205                 1210                 1215

Tyr Ser  Lys Phe Asp Ile Asn  Asn Ile Ile Lys Val  Asn Ser Trp
    1220                 1225                 1230

Asn Pro  Val Thr Asp Glu Val  Asn Asp Asp Asn Ile  Leu Thr Val
    1235                 1240                 1245

His Asn  Asp Thr Asn Gly Ala  Gln Tyr Met Gln Ser  Gly Gly Tyr
    1250                 1255                 1260

Arg Thr  Arg Leu Asn Thr Leu  Phe Ala Arg Lys Leu  Ile Ser Arg
    1265                 1270                 1275

Ala Thr  Ala Gly Ile Asp Thr  Ile Leu Asn Ile Glu  Thr Gln Lys
    1280                 1285                 1290
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Leu Pro  Glu Pro Gln Leu Gly  Lys Gly Phe Phe Thr  Asn Leu Ile
    1295                 1300                 1305

Leu Pro  Lys Tyr Asp Gln Asn  Val His Gly Ser Glu  Arg Trp Phe
    1310                 1315                 1320

Lys Ile  His Ile Arg Asn Asp  Asn Lys Met Met Asn  Leu Tyr His
    1325                 1330                 1335

Lys Gly  Thr Leu Thr Asp Thr  Glu Thr Ser Val Thr  Leu Phe Ile
    1340                 1345                 1350

Pro Trp  Ser Asn Thr Gln Glu  Arg Val Glu Ile Ala  Val Glu Tyr
    1355                 1360                 1365

Asn Lys  Lys Phe Tyr Lys Asp  Gln Gln Asn Trp Glu  Thr Ala Leu
    1370                 1375                 1380

Phe His  Phe Asn Glu Thr Asn  Gln Lys Phe Met Leu  Val Asn Asp
    1385                 1390                 1395

Ala Asp  Asn Lys Gln Val Val  Ile Asn Asp Thr Asp  Ala Ile Val
    1400                 1405                 1410

Asn Lys  Tyr Lys Gly Phe Leu  Asp Val Ser Ile Leu  Ile Asp Gln
    1415                 1420                 1425

His Thr  Glu Pro Met Asp Phe  Ser Gly Ala Asn Ser  Leu Tyr Phe
    1430                 1435                 1440

Trp Glu  Leu Phe Tyr Tyr Ala  Pro Met Leu Ile Ala  Gln Arg Leu
    1445                 1450                 1455

Leu His  Glu Gln His Phe Asp  Glu Ala Asn Arg Trp  Leu Lys Tyr
    1460                 1465                 1470

Ile Trp  Asn Pro Ser Gly Tyr  Ile Glu His Gly Gln  Ile Gln His
    1475                 1480                 1485

Tyr Arg  Trp Asn Val Arg Pro  Leu Leu Glu Asp Ile  Ser Trp Asn
    1490                 1495                 1500

Asp Asp  Pro Leu Asn Ser Val  Asp Pro Asp Ala Ile  Ala Gln Tyr
    1505                 1510                 1515

Asp Pro  Met His Tyr Lys Val  Val Thr Phe Met Arg  Thr Leu Asp
    1520                 1525                 1530

Leu Leu  Leu Asp Arg Gly Asp  Tyr Ala Tyr Arg Gln  Leu Glu Arg
    1535                 1540                 1545

Asp Thr  Leu Asn Glu Ala Lys  Met Trp Tyr Met Gln  Ala Leu His
    1550                 1555                 1560

Leu Leu  Gly Asp Lys Pro His  Leu Ser Phe Ser Ser  Thr Trp Arg
    1565                 1570                 1575

Lys Pro  Ser Leu Gly Asp Ala  Ala Arg Thr Glu Lys  Gln Glu Glu
    1580                 1585                 1590

Gln Ala  His Ala Met Thr Ala  Leu Arg Gln Gly Asp  Ile Ser Arg
    1595                 1600                 1605

His Asn  His Pro Thr Asp Leu  Phe Leu Pro Gln Val  Asn Glu Val
    1610                 1615                 1620

Met Gln  Asn Tyr Trp Gln Lys  Leu Glu Gln Arg Leu  Tyr Asn Leu
    1625                 1630                 1635

Arg His  Asn Leu Ser Ile Asp  Gly Gln Leu Leu His  Leu Pro Ile
    1640                 1645                 1650

Tyr Ala  Thr Pro Ala Asp Pro  Lys Ala Leu Leu Ser  Ala Ala Val
    1655                 1660                 1665

Ala Asn  Ser Gln Gly Gly Ser  Lys Leu Pro Met Ser  Phe Met Ser
    1670                 1675                 1680

Leu Trp  Arg Phe Pro Gln Met  Leu Glu Asn Ala Arg  Gly Met Val
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    1685                 1690                 1695

Ser Gln  Leu Thr Gln Phe Gly  Ser Thr Leu Gln Asn  Ile Ile Glu
    1700                 1705                 1710

Arg Gln  Asp Ala Glu Ala Leu  Asn Thr Leu Leu Gln  Asn Gln Ala
    1715                 1720                 1725

Ala Glu  Leu Ile Leu Thr Asn  Leu Ser Ile Gln Asp  Lys Thr Leu
    1730                 1735                 1740

Glu Glu  Leu Asp Ala Glu Lys  Ile Val Leu Glu Lys  Ser Lys Ala
    1745                 1750                 1755

Gly Ala  Gln Ser Arg Phe Asn  Ser Tyr Lys Lys Leu  Tyr Asp Glu
    1760                 1765                 1770

Asn Ile  Asn Ala Gly Glu Asn  Arg Val Ile Ala Leu  His Ser Ser
    1775                 1780                 1785

Val Ala  Gly Leu Ser Thr Ala  Leu Gln Ala Ser Arg  Leu Ala Gly
    1790                 1795                 1800

Ala Ala  Leu Asp Leu Ala Pro  Asn Ile Phe Gly Phe  Ala Asp Gly
    1805                 1810                 1815

Gly Ser  Arg Trp Gly Ala Ile  Ala Glu Ala Thr Gly  Asn Val Met
    1820                 1825                 1830

Glu Phe  Ser Ala Asn Val Met  Asn Thr Glu Ala Asp  Lys Ile Ser
    1835                 1840                 1845

Gln Ser  Glu Thr Tyr Arg Arg  Arg Arg Gln Glu Trp  Glu Ile Gln
    1850                 1855                 1860

Arg Asn  Asn Ala Glu Ala Glu  Ile Lys Gln Ile Asp  Ala Gln Leu
    1865                 1870                 1875

Gln Ser  Leu Ala Val Arg Arg  Glu Ala Ala Val Leu  Gln Lys Thr
    1880                 1885                 1890

Ser Leu  Lys Thr Gln Gln Glu  Gln Thr Gln Ala Gln  Leu Thr Phe
    1895                 1900                 1905

Leu Gln  Arg Lys Phe Ser Asn  Gln Ala Leu Tyr His  Trp Leu Arg
    1910                 1915                 1920

Gly Arg  Leu Ala Ala Ile Tyr  Phe Gln Phe Tyr Asp  Leu Ala Val
    1925                 1930                 1935

Thr Arg  Cys Leu Met Ala Glu  Met Ala Tyr Arg Trp  Glu Thr His
    1940                 1945                 1950

Asn Thr  Thr Ala Ser Phe Ile  Lys Pro Gly Ala Trp  Gln Gly Thr
    1955                 1960                 1965

His Ala  Gly Leu Leu Ala Gly  Glu Thr Leu Met Leu  Asn Leu Ala
    1970                 1975                 1980

Gln Met  Glu Asp Ala Tyr Leu  Arg Trp Asp Gln Arg  Ala Leu Glu
    1985                 1990                 1995

Val Glu  Arg Thr Ile Ser Leu  Ala Gln Leu Tyr Gly  Thr Leu Pro
    2000                 2005                 2010

Glu Lys  Ser Phe Asn Leu Ala  Thr Arg Ile Ser Ala  Leu Leu Thr
    2015                 2020                 2025

Gly Ser  Thr Thr Glu Pro Val  Glu Glu His Pro Val  Thr Leu Glu
    2030                 2035                 2040

Asn Gly  Gln Leu Ser Ala Lys  Ile Ser Leu Ser Gly  Leu Ser Leu
    2045                 2050                 2055

His Asn  Asp Tyr Pro Glu Gly  Asn Gly Val Gly Asn  Ile Arg Arg
    2060                 2065                 2070

Ile Lys  Gln Ile Ser Val Thr  Leu Pro Ala Leu Leu  Gly Pro Tyr
    2075                 2080                 2085
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Gln Asn  Val Gln Ala Ile Leu  Ala Tyr Glu Gly Ser  Glu Ile Gly
    2090                 2095                 2100

Leu Ala  Glu Ser Cys Lys Ser  Leu Ala Ile Ser His  Gly Val Asn
    2105                 2110                 2115

Asp Ser  Gly Gln Phe Gln Leu  Asp Phe Asn Asn Gly  Lys Phe Leu
    2120                 2125                 2130

Pro Phe  Glu Gly Ile Ala Ile  Asn Asp Thr Gly Thr  Leu Thr Leu
    2135                 2140                 2145

Asn Phe  Pro Asn Ala Thr Gly  Lys Gln Gln Ala Met  Leu Gln Ala
    2150                 2155                 2160

Leu Ser  Asp Ile Ile Leu His  Ile Arg Tyr Thr Ile  Arg Gln
    2165                 2170                 2175


<210> SEQ ID NO 7
<211> LENGTH: 7146
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<213> ORGANISM: Photorhabdus luminescens
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Met Asn Ser Tyr Val Lys Glu Ile Pro Asp Val Leu Gln Ser Gln Tyr
1               5                   10                  15

ggt att aat tgt ctg aca gat att tgc cac tat tct ttt aat gaa ttt       96
Gly Ile Asn Cys Leu Thr Asp Ile Cys His Tyr Ser Phe Asn Glu Phe
            20                  25                  30

cgt cag caa gtc tct gat cat ctc tcc tgg tca gag acc aac cgc tta      144
Arg Gln Gln Val Ser Asp His Leu Ser Trp Ser Glu Thr Asn Arg Leu
        35                  40                  45

tat cgt gat gca caa cag gaa caa aaa gag aat caa tta tat gaa gct      192
Tyr Arg Asp Ala Gln Gln Glu Gln Lys Glu Asn Gln Leu Tyr Glu Ala
    50                  55                  60

cgt att ctt aaa cgc gct aac ccg cag ttg caa aat gca gtg cac ctc      240
Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65                  70                  75                  80

ggt att acc ctc cct cat gct gaa tta cga ggc tat aat agt gaa ttc      288
Gly Ile Thr Leu Pro His Ala Glu Leu Arg Gly Tyr Asn Ser Glu Phe
                85                  90                  95

ggt ggc cga gcc agc caa tat gtg gcg ccg ggt tcg gtt tcc tct atg      336
Gly Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Ser Val Ser Ser Met
            100                 105                 110

ttc tcc ccc gca gct tat tta act gaa ctc tat cgt gaa gca cgt aat      384
Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
        115                 120                 125

tta cat gcc agc gac tcc gtt tat cat ctg gat gaa cgc cgc cca gac      432
Leu His Ala Ser Asp Ser Val Tyr His Leu Asp Glu Arg Arg Pro Asp
    130                 135                 140

ctc caa tca atg acg ctc agc cag caa aat atg gat acc gaa ctt tcc      480
Leu Gln Ser Met Thr Leu Ser Gln Gln Asn Met Asp Thr Glu Leu Ser
145                 150                 155                 160

act ctt tct ctg tct aat gaa att ttg ttg aaa gga att aaa gct aat      528
Thr Leu Ser Leu Ser Asn Glu Ile Leu Leu Lys Gly Ile Lys Ala Asn
                165                 170                 175

cag tct aat ctg gac agc gat act aag gtg atg gaa atg tta tcc act      576
Gln Ser Asn Leu Asp Ser Asp Thr Lys Val Met Glu Met Leu Ser Thr
            180                 185                 190

ttc cgt cct tcc ggc acg ata cct tat cat gat gct tac gaa aat gta      624
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Phe Arg Pro Ser Gly Thr Ile Pro Tyr His Asp Ala Tyr Glu Asn Val
        195                 200                 205

cgt aaa gct atc caa tta caa gat ccg aaa ctt gaa caa ttt cag aaa      672
Arg Lys Ala Ile Gln Leu Gln Asp Pro Lys Leu Glu Gln Phe Gln Lys
    210                 215                 220

tca ccg gcg gtc gcc gga tta atg cat caa gct tca tta tta gga att      720
Ser Pro Ala Val Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile
225                 230                 235                 240

aat aac tct atc tca cca gaa ctg ttt aat att ctg aca gaa gag att      768
Asn Asn Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile
                245                 250                 255

acc gaa gct aac gca gag gca att tat aaa cag aat ttt ggc gat att      816
Thr Glu Ala Asn Ala Glu Ala Ile Tyr Lys Gln Asn Phe Gly Asp Ile
            260                 265                 270

gac cct gcc tgc ctg gca atg ccg gaa tat ctg aaa agt tat tat aat      864
Asp Pro Ala Cys Leu Ala Met Pro Glu Tyr Leu Lys Ser Tyr Tyr Asn
        275                 280                 285

ttt agt gat gaa gaa ctc agt caa ttt att cgc aaa tat cca gat aat      912
Phe Ser Asp Glu Glu Leu Ser Gln Phe Ile Arg Lys Tyr Pro Asp Asn
    290                 295                 300

gaa cta aat act cag aaa ata cat tta cta aaa atc aat aaa att att      960
Glu Leu Asn Thr Gln Lys Ile His Leu Leu Lys Ile Asn Lys Ile Ile
305                 310                 315                 320

tta tta tcg caa gcc gtg aat ctg ccg ttt tta aag tta gat gaa att     1008
Leu Leu Ser Gln Ala Val Asn Leu Pro Phe Leu Lys Leu Asp Glu Ile
                325                 330                 335

att cca gaa cag aac att acc ccg aca gta tta ggg aaa atc ttt cta     1056
Ile Pro Glu Gln Asn Ile Thr Pro Thr Val Leu Gly Lys Ile Phe Leu
            340                 345                 350

gtt aaa tat tat atg cag aaa tac aat att ggt acg gaa act gcc tta     1104
Val Lys Tyr Tyr Met Gln Lys Tyr Asn Ile Gly Thr Glu Thr Ala Leu
        355                 360                 365

ata tta tgt aat gat tcc att tca caa tac tcc tat agt aat caa cct     1152
Ile Leu Cys Asn Asp Ser Ile Ser Gln Tyr Ser Tyr Ser Asn Gln Pro
    370                 375                 380

agc caa ttt gat cgc cta ttt aat acc tcg cca ctc aat gga caa tat     1200
Ser Gln Phe Asp Arg Leu Phe Asn Thr Ser Pro Leu Asn Gly Gln Tyr
385                 390                 395                 400

ttc gtt atc gaa gac act aat att gac cta agt ctg aac agt acc gat     1248
Phe Val Ile Glu Asp Thr Asn Ile Asp Leu Ser Leu Asn Ser Thr Asp
                405                 410                 415

aac tgg cac aaa gca gta ctt aaa cgt gct ttt aat gtc gat gat att     1296
Asn Trp His Lys Ala Val Leu Lys Arg Ala Phe Asn Val Asp Asp Ile
            420                 425                 430

tcc ctc tat cgt tta ctc cat att gcc aat cat aac aat acc gat gga     1344
Ser Leu Tyr Arg Leu Leu His Ile Ala Asn His Asn Asn Thr Asp Gly
        435                 440                 445

aaa att gct aat aat ata aaa aat ctt tcc aat ctt tat atg act aaa     1392
Lys Ile Ala Asn Asn Ile Lys Asn Leu Ser Asn Leu Tyr Met Thr Lys
    450                 455                 460

cta ctg gca gat att cat caa tta acg att gat gaa ctg tat tta cta     1440
Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Tyr Leu Leu
465                 470                 475                 480

ctg ata act att ggt gaa gat aaa ata aat tta tat gat att gat gat     1488
Leu Ile Thr Ile Gly Glu Asp Lys Ile Asn Leu Tyr Asp Ile Asp Asp
                485                 490                 495

aaa gag ctg gag aaa ctc ata aac aga ctc gat acc cta agc aat tgg     1536
Lys Glu Leu Glu Lys Leu Ile Asn Arg Leu Asp Thr Leu Ser Asn Trp
            500                 505                 510
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ctg cat aca caa aag tgg agt atc tat cag tta ttt ttg atg acc acc     1584
Leu His Thr Gln Lys Trp Ser Ile Tyr Gln Leu Phe Leu Met Thr Thr
        515                 520                 525

acc aac tat gac aaa aca cta acg cct gaa att caa aac tta ctc gat     1632
Thr Asn Tyr Asp Lys Thr Leu Thr Pro Glu Ile Gln Asn Leu Leu Asp
    530                 535                 540

acg gtc tac aat ggc tta cag aac ttc gat aaa aat aaa acc aaa ctt     1680
Thr Val Tyr Asn Gly Leu Gln Asn Phe Asp Lys Asn Lys Thr Lys Leu
545                 550                 555                 560

ctg gca gcc atc gcg cct tat att gct gca aca cta caa tta cca tct     1728
Leu Ala Ala Ile Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Pro Ser
                565                 570                 575

gaa aat gtc gca cat tct att ctt ctc tgg gct gat aag ata aaa cca     1776
Glu Asn Val Ala His Ser Ile Leu Leu Trp Ala Asp Lys Ile Lys Pro
            580                 585                 590

agc gaa aat aaa ata acg gca gaa aaa ttt tgg atc tgg tta caa aat     1824
Ser Glu Asn Lys Ile Thr Ala Glu Lys Phe Trp Ile Trp Leu Gln Asn
        595                 600                 605

aga gat act aca gaa ttg tca aaa ccg cca gaa atg cag gaa caa att     1872
Arg Asp Thr Thr Glu Leu Ser Lys Pro Pro Glu Met Gln Glu Gln Ile
    610                 615                 620

att cag tac tgc cac tgt ctg gca caa ttg aca atg att tat cgt tct     1920
Ile Gln Tyr Cys His Cys Leu Ala Gln Leu Thr Met Ile Tyr Arg Ser
625                 630                 635                 640

tcc ggc att aat gaa aac gct ttc cgt cta ttt atc gaa aag cca act     1968
Ser Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Ile Glu Lys Pro Thr
                645                 650                 655

att ttt ggc atc cct gat gaa ccg aat aaa gcg aca cca gcc cat aat     2016
Ile Phe Gly Ile Pro Asp Glu Pro Asn Lys Ala Thr Pro Ala His Asn
            660                 665                 670

gca cca aca tta atc atc cta acc cgc ttt gcc aat tgg gtt aat tct     2064
Ala Pro Thr Leu Ile Ile Leu Thr Arg Phe Ala Asn Trp Val Asn Ser
        675                 680                 685

cta ggt gaa aaa gcc tcc cct att cta acg gct ttt gaa aat aaa acc     2112
Leu Gly Glu Lys Ala Ser Pro Ile Leu Thr Ala Phe Glu Asn Lys Thr
    690                 695                 700

tta act gcg gaa aaa tta gct aac gcc atg aat ctt gat gct aat tta     2160
Leu Thr Ala Glu Lys Leu Ala Asn Ala Met Asn Leu Asp Ala Asn Leu
705                 710                 715                 720

ctg gaa caa gcc agt att caa gca caa aat tat aag cag gtt act aaa     2208
Leu Glu Gln Ala Ser Ile Gln Ala Gln Asn Tyr Lys Gln Val Thr Lys
                725                 730                 735

gaa aat aca ttc tcc aat tgg caa tcc atc gac att att ctg caa tgg     2256
Glu Asn Thr Phe Ser Asn Trp Gln Ser Ile Asp Ile Ile Leu Gln Trp
            740                 745                 750

act aat ata gcc agt aat tta aat atc tcc cca caa ggt att tcc cct     2304
Thr Asn Ile Ala Ser Asn Leu Asn Ile Ser Pro Gln Gly Ile Ser Pro
        755                 760                 765

cta ata gca ttg gat tat ata aaa ccg gct caa aaa aca ccg act tat     2352
Leu Ile Ala Leu Asp Tyr Ile Lys Pro Ala Gln Lys Thr Pro Thr Tyr
    770                 775                 780

gcc caa tgg gaa aat gca gct ata gca tta act gcc ggg tta gac act     2400
Ala Gln Trp Glu Asn Ala Ala Ile Ala Leu Thr Ala Gly Leu Asp Thr
785                 790                 795                 800

caa caa act cat act cta cac gta ttt ctg gac gaa tct cgc agt acc     2448
Gln Gln Thr His Thr Leu His Val Phe Leu Asp Glu Ser Arg Ser Thr
                805                 810                 815

gca tta agc aac tat tat att ggc aag gtt gct aat cgg gca gca tca     2496
Ala Leu Ser Asn Tyr Tyr Ile Gly Lys Val Ala Asn Arg Ala Ala Ser
            820                 825                 830
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att aaa agc cgt gac gat tta tac caa tac tta ctg att gat aat caa     2544
Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln
        835                 840                 845

gtt tcc gct gaa ata aaa act aca cgt att gcc gaa gcc att gcc agt     2592
Val Ser Ala Glu Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser
    850                 855                 860

atc caa ttg tat gtc aac cga gcg ctg gaa aat ata gaa atc cat gcc     2640
Ile Gln Leu Tyr Val Asn Arg Ala Leu Glu Asn Ile Glu Ile His Ala
865                 870                 875                 880

gtt tct gat gtt att acc cgt caa ttt ttt atc gat tgg gat aaa tat     2688
Val Ser Asp Val Ile Thr Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr
                885                 890                 895

aat aaa cgt tac agt act tgg gct ggc gtt tca caa tta gtt tac tat     2736
Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr
            900                 905                 910

ccc gaa aat tat atc gac ccg acg atg cgt atc gga caa acg aaa atg     2784
Pro Glu Asn Tyr Ile Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met
        915                 920                 925

atg gat acg tta ttg caa tcc gtc agc cag agc caa tta aat gcc gat     2832
Met Asp Thr Leu Leu Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp
    930                 935                 940

acg gta gaa gat gca ttt aaa tct tac ctg acc tcg ttt gaa caa gtc     2880
Thr Val Glu Asp Ala Phe Lys Ser Tyr Leu Thr Ser Phe Glu Gln Val
945                 950                 955                 960

gct aat ttg gaa gtc att agt gct tat cat gat aac gtt aat aat gac     2928
Ala Asn Leu Glu Val Ile Ser Ala Tyr His Asp Asn Val Asn Asn Asp
                965                 970                 975

caa gga ctg acc tat ttt atc ggg aac agc aaa aca gaa gtt aat caa     2976
Gln Gly Leu Thr Tyr Phe Ile Gly Asn Ser Lys Thr Glu Val Asn Gln
            980                 985                 990

tat tac tgg cgc agc gtc gat cac  agt aaa ttc aac gac  ggt aaa ttc   3024
Tyr Tyr Trp Arg Ser Val Asp His  Ser Lys Phe Asn Asp  Gly Lys Phe
        995                 1000                 1005

gct gct  aat gcc tgg agt gaa  tgg cac aaa att gac  tgc gca att      3069
Ala Ala  Asn Ala Trp Ser Glu  Trp His Lys Ile Asp  Cys Ala Ile
    1010                 1015                 1020

aat ccc  tac caa agc acc att  cgc cca gtt atc tat  aaa tcc cga      3114
Asn Pro  Tyr Gln Ser Thr Ile  Arg Pro Val Ile Tyr  Lys Ser Arg
    1025                 1030                 1035

tta tat  ctg att tgg ctg gaa  caa aaa gaa aca gct  aaa caa aag      3159
Leu Tyr  Leu Ile Trp Leu Glu  Gln Lys Glu Thr Ala  Lys Gln Lys
    1040                 1045                 1050

gag gat  aat aaa gtc act aca  gac tat cac tat gaa  tta aaa ttg      3204
Glu Asp  Asn Lys Val Thr Thr  Asp Tyr His Tyr Glu  Leu Lys Leu
    1055                 1060                 1065

gct cat  att cgt tat gat ggt  acc tgg aat gtg cca  atc acc ttt      3249
Ala His  Ile Arg Tyr Asp Gly  Thr Trp Asn Val Pro  Ile Thr Phe
    1070                 1075                 1080

gat gta  gat gaa aaa ata cta  gct tta gaa ctg aca  aaa tct caa      3294
Asp Val  Asp Glu Lys Ile Leu  Ala Leu Glu Leu Thr  Lys Ser Gln
    1085                 1090                 1095

gca cct  gga ctc tat tgc gca  ggt tat caa ggg gaa  gat aca cta      3339
Ala Pro  Gly Leu Tyr Cys Ala  Gly Tyr Gln Gly Glu  Asp Thr Leu
    1100                 1105                 1110

tta atc  atg ttt tat aga aaa  aaa gag aaa ttg gat  gat tat aaa      3384
Leu Ile  Met Phe Tyr Arg Lys  Lys Glu Lys Leu Asp  Asp Tyr Lys
    1115                 1120                 1125

act gca  cca atg caa gga ttt  tat att ttc tcc gat  atg tct tcc      3429
Thr Ala  Pro Met Gln Gly Phe  Tyr Ile Phe Ser Asp  Met Ser Ser
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    1130                1135                1140

aaa gat  atg acc aat gaa caa  tgc aat tct tat cga  gat aac ggt      3474
Lys Asp  Met Thr Asn Glu Gln  Cys Asn Ser Tyr Arg  Asp Asn Gly
    1145                1150                1155

tat aca  cat ttc gat act aat  tct gat act aat agc  gtc ata aga      3519
Tyr Thr  His Phe Asp Thr Asn  Ser Asp Thr Asn Ser  Val Ile Arg
    1160                1165                1170

ata aat  aat cgc tat gca gag  gat tat gaa att cct  tca ttg atc      3564
Ile Asn  Asn Arg Tyr Ala Glu  Asp Tyr Glu Ile Pro  Ser Leu Ile
    1175                1180                1185

aat cat  agc aat agc cat gat  tgg ggg gaa tat aat  ctt agc cag      3609
Asn His  Ser Asn Ser His Asp  Trp Gly Glu Tyr Asn  Leu Ser Gln
    1190                1195                1200

gta tat  ggc gga aat ata gtt  atc aat tac aaa gtt  aca tca aat      3654
Val Tyr  Gly Gly Asn Ile Val  Ile Asn Tyr Lys Val  Thr Ser Asn
    1205                1210                1215

gat ttg  aaa atc tat att tca  cca aaa tta aga ata  atc cat gat      3699
Asp Leu  Lys Ile Tyr Ile Ser  Pro Lys Leu Arg Ile  Ile His Asp
    1220                1225                1230

gga aaa  gaa ggt cga gag cgc  att cag tct aat cta  ata aag aaa      3744
Gly Lys  Glu Gly Arg Glu Arg  Ile Gln Ser Asn Leu  Ile Lys Lys
    1235                1240                1245

tac ggc  aaa ttg ggt gat aaa  ttc att att tat act  agt ttg gga      3789
Tyr Gly  Lys Leu Gly Asp Lys  Phe Ile Ile Tyr Thr  Ser Leu Gly
    1250                1255                1260

atc aat  ccg aat aat tca tca  aat aga ttc atg ttt  tac cca gtc      3834
Ile Asn  Pro Asn Asn Ser Ser  Asn Arg Phe Met Phe  Tyr Pro Val
    1265                1270                1275

tat caa  tat aat gga aac act  agc ggc ctt gct caa  ggg aga cta      3879
Tyr Gln  Tyr Asn Gly Asn Thr  Ser Gly Leu Ala Gln  Gly Arg Leu
    1280                1285                1290

tta ttc  cat cga gac acg agt  tat tca tct aaa gta  gcg gct tgg      3924
Leu Phe  His Arg Asp Thr Ser  Tyr Ser Ser Lys Val  Ala Ala Trp
    1295                1300                1305

att cct  ggg gca gga cgt tct  tta atc aat gaa aat  gct aac atc      3969
Ile Pro  Gly Ala Gly Arg Ser  Leu Ile Asn Glu Asn  Ala Asn Ile
    1310                1315                1320

ggt gat  gat tgt gct gaa gat  tct gtg aat aaa ccg  gat gat ctt      4014
Gly Asp  Asp Cys Ala Glu Asp  Ser Val Asn Lys Pro  Asp Asp Leu
    1325                1330                1335

aag caa  tac atc tat atg act  gac agt aaa ggg act  gct act gat      4059
Lys Gln  Tyr Ile Tyr Met Thr  Asp Ser Lys Gly Thr  Ala Thr Asp
    1340                1345                1350

gtt tcc  ggg cca gta gat atc  aac aca gca att tct  tct gaa aag      4104
Val Ser  Gly Pro Val Asp Ile  Asn Thr Ala Ile Ser  Ser Glu Lys
    1355                1360                1365

gtt caa  atc aca att aaa gct  ggc aaa gaa tac tct  ctt aca gcg      4149
Val Gln  Ile Thr Ile Lys Ala  Gly Lys Glu Tyr Ser  Leu Thr Ala
    1370                1375                1380

aat aaa  gat gtc tcc gtt cag  cca tca cct agc ttt  gaa gaa atg      4194
Asn Lys  Asp Val Ser Val Gln  Pro Ser Pro Ser Phe  Glu Glu Met
    1385                1390                1395

tgt tac  caa ttt aat gct ctc  gaa ata gat ggc tct  aat ctg aat      4239
Cys Tyr  Gln Phe Asn Ala Leu  Glu Ile Asp Gly Ser  Asn Leu Asn
    1400                1405                1410

ttt act  aac aat tca gcc agt  att gat gtc act ttt  acc gca ctg      4284
Phe Thr  Asn Asn Ser Ala Ser  Ile Asp Val Thr Phe  Thr Ala Leu
    1415                1420                1425

gca gat  gat gga cgc aaa ttg  ggt tat gaa att ttc  aat atc cct      4329
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Ala Asp  Asp Gly Arg Lys Leu  Gly Tyr Glu Ile Phe  Asn Ile Pro
    1430                 1435                 1440

gtt att  caa aag gtt aaa acc  gat aat gct cta act  ctt ttt cat      4374
Val Ile  Gln Lys Val Lys Thr  Asp Asn Ala Leu Thr  Leu Phe His
    1445                 1450                 1455

gac gag  aat ggc gct caa tat  atg caa tgg gga gcc  tat cgc att      4419
Asp Glu  Asn Gly Ala Gln Tyr  Met Gln Trp Gly Ala  Tyr Arg Ile
    1460                 1465                 1470

cgc ctt  aat acg cta ttt gct  cgc caa tta gtt gaa  cga gct aat      4464
Arg Leu  Asn Thr Leu Phe Ala  Arg Gln Leu Val Glu  Arg Ala Asn
    1475                 1480                 1485

act ggt  att gat aca att cta  agt atg gaa act cag  aat att cag      4509
Thr Gly  Ile Asp Thr Ile Leu  Ser Met Glu Thr Gln  Asn Ile Gln
    1490                 1495                 1500

gaa ccg  atg atg gga ata ggc  gct tat ata gaa ctc  att ttg gat      4554
Glu Pro  Met Met Gly Ile Gly  Ala Tyr Ile Glu Leu  Ile Leu Asp
    1505                 1510                 1515

aaa tat  aat cct gat atc cac  ggc act aat aaa tca  ttt aag att      4599
Lys Tyr  Asn Pro Asp Ile His  Gly Thr Asn Lys Ser  Phe Lys Ile
    1520                 1525                 1530

ata tat  ggt gat att ttt aaa  gca ggt gat cat ttt  cct att tat      4644
Ile Tyr  Gly Asp Ile Phe Lys  Ala Gly Asp His Phe  Pro Ile Tyr
    1535                 1540                 1545

cag gga  gca tta agc gat att  aca caa aca aca gta  aaa tta ttc      4689
Gln Gly  Ala Leu Ser Asp Ile  Thr Gln Thr Thr Val  Lys Leu Phe
    1550                 1555                 1560

tta cct  cgc gtt gat aac gct  tat gga aat aaa aac  aat ctc tat      4734
Leu Pro  Arg Val Asp Asn Ala  Tyr Gly Asn Lys Asn  Asn Leu Tyr
    1565                 1570                 1575

gtt tac  gcg gcc tat caa aaa  gtg gaa aca aat ttc  att cga ttc      4779
Val Tyr  Ala Ala Tyr Gln Lys  Val Glu Thr Asn Phe  Ile Arg Phe
    1580                 1585                 1590

gtt aaa  gag gat aat aat aaa  ccc gct aca ttc gac  act acc tat      4824
Val Lys  Glu Asp Asn Asn Lys  Pro Ala Thr Phe Asp  Thr Thr Tyr
    1595                 1600                 1605

aag aat  ggg acc ttc cca ggg  ctt gca tca gcc aga  gta ata caa      4869
Lys Asn  Gly Thr Phe Pro Gly  Leu Ala Ser Ala Arg  Val Ile Gln
    1610                 1615                 1620

act gtc  tcg gaa cca atg gat  ttc agc ggc gct aat  agt ctc tac      4914
Thr Val  Ser Glu Pro Met Asp  Phe Ser Gly Ala Asn  Ser Leu Tyr
    1625                 1630                 1635

ttc tgg  gaa ctg ttc tac tat  acc ccg atg atg gtt  gct caa cgt      4959
Phe Trp  Glu Leu Phe Tyr Tyr  Thr Pro Met Met Val  Ala Gln Arg
    1640                 1645                 1650

ttg cta  cat gaa caa aac ttt  gat gaa gcc aac cgt  tgg cta aaa      5004
Leu Leu  His Glu Gln Asn Phe  Asp Glu Ala Asn Arg  Trp Leu Lys
    1655                 1660                 1665

tat gtc  tgg agc cca tcc ggt  tat att gtt cga ggt  caa att aaa      5049
Tyr Val  Trp Ser Pro Ser Gly  Tyr Ile Val Arg Gly  Gln Ile Lys
    1670                 1675                 1680

aac tac  cac tgg aat gtg cgc  cca tta ctg gaa aac  acc agt tgg      5094
Asn Tyr  His Trp Asn Val Arg  Pro Leu Leu Glu Asn  Thr Ser Trp
    1685                 1690                 1695

aac agt  gat cct ttg gat tcc  gtc gat cct gac gca  gtg gca cag      5139
Asn Ser  Asp Pro Leu Asp Ser  Val Asp Pro Asp Ala  Val Ala Gln
    1700                 1705                 1710

cac gat  cca atg cac tat aaa  gta gcc acc ttt atg  cgt act ctc      5184
His Asp  Pro Met His Tyr Lys  Val Ala Thr Phe Met  Arg Thr Leu
    1715                 1720                 1725
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gat cta  ctg atg gca cgc ggc  gat cac gcc tat cgc  caa ctt gag      5229
Asp Leu  Leu Met Ala Arg Gly  Asp His Ala Tyr Arg  Gln Leu Glu
    1730                 1735                 1740

cgg gat  acg ctg aac gaa gcc  aaa atg tgg tat atg  caa gca ctg      5274
Arg Asp  Thr Leu Asn Glu Ala  Lys Met Trp Tyr Met  Gln Ala Leu
    1745                 1750                 1755

cac ctg  ttg ggc aat aaa ccc  tat ctg cct ctg agt  tct gta tgg      5319
His Leu  Leu Gly Asn Lys Pro  Tyr Leu Pro Leu Ser  Ser Val Trp
    1760                 1765                 1770

aat gat  cca cgt ctg gac aat  gcc gca gcc act acc  aca caa aaa      5364
Asn Asp  Pro Arg Leu Asp Asn  Ala Ala Ala Thr Thr  Thr Gln Lys
    1775                 1780                 1785

gca cac  gcc tac gca ata acc  tct cta cgg caa ggc  acg caa aca      5409
Ala His  Ala Tyr Ala Ile Thr  Ser Leu Arg Gln Gly  Thr Gln Thr
    1790                 1795                 1800

cca gca  tta tta ttg cgc tcc  gct aat acc ctg acc  gat ctt ttc      5454
Pro Ala  Leu Leu Leu Arg Ser  Ala Asn Thr Leu Thr  Asp Leu Phe
    1805                 1810                 1815

ctg cca  caa atc aac gac gtt  atg ttg agc tac tgg  aac aaa ctg      5499
Leu Pro  Gln Ile Asn Asp Val  Met Leu Ser Tyr Trp  Asn Lys Leu
    1820                 1825                 1830

gaa ctg  cgt ctg tat aac tta  cgt cat aat ctc tct  atc gat ggt      5544
Glu Leu  Arg Leu Tyr Asn Leu  Arg His Asn Leu Ser  Ile Asp Gly
    1835                 1840                 1845

cag cct  ctc cac cta ccg att  tac gcc aca ccg gcc  gat ccg aaa      5589
Gln Pro  Leu His Leu Pro Ile  Tyr Ala Thr Pro Ala  Asp Pro Lys
    1850                 1855                 1860

gcg tta  ctc agc gcc gcc gtt  gct act tct caa ggc  ggc ggc aaa      5634
Ala Leu  Leu Ser Ala Ala Val  Ala Thr Ser Gln Gly  Gly Gly Lys
    1865                 1870                 1875

cta cca  gag tca ttt ata tca  ctg tgg cgc ttc ccg  cat atg ttg      5679
Leu Pro  Glu Ser Phe Ile Ser  Leu Trp Arg Phe Pro  His Met Leu
    1880                 1885                 1890

gaa aat  gcc cgt agt atg gtc  act cag cta ata cag  ttc ggc tcc      5724
Glu Asn  Ala Arg Ser Met Val  Thr Gln Leu Ile Gln  Phe Gly Ser
    1895                 1900                 1905

acg ttg  caa aat att att gaa  cgc caa gat gct gaa  tcc tta aat      5769
Thr Leu  Gln Asn Ile Ile Glu  Arg Gln Asp Ala Glu  Ser Leu Asn
    1910                 1915                 1920

gct ctg  ctg caa aat caa gcc  aaa gag ttg att ttg  aca acg ctc      5814
Ala Leu  Leu Gln Asn Gln Ala  Lys Glu Leu Ile Leu  Thr Thr Leu
    1925                 1930                 1935

agc att  caa gac aaa acc atc  gaa gaa ata gat gct  gaa aaa act      5859
Ser Ile  Gln Asp Lys Thr Ile  Glu Glu Ile Asp Ala  Glu Lys Thr
    1940                 1945                 1950

gtg ctg  gaa aaa tcc aaa gcc  gga gca aaa tcg cgc  ttt gac aac      5904
Val Leu  Glu Lys Ser Lys Ala  Gly Ala Lys Ser Arg  Phe Asp Asn
    1955                 1960                 1965

tac agc  aaa tta tat gac gaa  gat gtc aac gcc ggt  gag cgt caa      5949
Tyr Ser  Lys Leu Tyr Asp Glu  Asp Val Asn Ala Gly  Glu Arg Gln
    1970                 1975                 1980

gct ctg  gat atg cga ata gct  tcc caa agt att acc  tca gga ttg      5994
Ala Leu  Asp Met Arg Ile Ala  Ser Gln Ser Ile Thr  Ser Gly Leu
    1985                 1990                 1995

aaa ggc  ttg cac atg gct gcc  gcc gca ctg gag atg  gtg ccc aat      6039
Lys Gly  Leu His Met Ala Ala  Ala Ala Leu Glu Met  Val Pro Asn
    2000                 2005                 2010

atc tac  ggc ttt gca gtc ggg  ggg acg cgc tat gga  gca att gcc      6084
Ile Tyr  Gly Phe Ala Val Gly  Gly Thr Arg Tyr Gly  Ala Ile Ala
    2015                 2020                 2025
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aat gcc  att gcg att ggt ggc  ggt atc gcc gca gaa  ggt ttg tta      6129
Asn Ala  Ile Ala Ile Gly Gly  Gly Ile Ala Ala Glu  Gly Leu Leu
    2030                 2035                 2040

att gaa  gca gag aaa gtc tcg  caa tct gaa ata tgg  cgc cgt cgc      6174
Ile Glu  Ala Glu Lys Val Ser  Gln Ser Glu Ile Trp  Arg Arg Arg
    2045                 2050                 2055

cgt caa  gag tgg gaa atc cag  cgt aat aat gcc gaa  gca gag atg      6219
Arg Gln  Glu Trp Glu Ile Gln  Arg Asn Asn Ala Glu  Ala Glu Met
    2060                 2065                 2070

aaa caa  atc gat gct caa ctt  aaa tca cta acg gta  cgc cgt gaa      6264
Lys Gln  Ile Asp Ala Gln Leu  Lys Ser Leu Thr Val  Arg Arg Glu
    2075                 2080                 2085

gcg gcg  gta tta cag aaa acc  ggc cta aaa acc caa  cag gaa caa      6309
Ala Ala  Val Leu Gln Lys Thr  Gly Leu Lys Thr Gln  Gln Glu Gln
    2090                 2095                 2100

act caa  gcg caa cta gct ttc  ctg caa cga aaa ttc  agc aat caa      6354
Thr Gln  Ala Gln Leu Ala Phe  Leu Gln Arg Lys Phe  Ser Asn Gln
    2105                 2110                 2115

gcg ctg  tat aat tgg tta cgt  ggt cgg tta gca gcc  att tat ttc      6399
Ala Leu  Tyr Asn Trp Leu Arg  Gly Arg Leu Ala Ala  Ile Tyr Phe
    2120                 2125                 2130

caa ttt  tac gat tta gtc gtc  gcc cgt tgt ttg atg  gca gaa caa      6444
Gln Phe  Tyr Asp Leu Val Val  Ala Arg Cys Leu Met  Ala Glu Gln
    2135                 2140                 2145

gct tac  cgt tgg gaa act aat  gat agc tct gca cgc  ttt att aaa      6489
Ala Tyr  Arg Trp Glu Thr Asn  Asp Ser Ser Ala Arg  Phe Ile Lys
    2150                 2155                 2160

ccg gga  gcc tgg cag gga acc  tat gcc ggc ctg ctc  gcc gga gaa      6534
Pro Gly  Ala Trp Gln Gly Thr  Tyr Ala Gly Leu Leu  Ala Gly Glu
    2165                 2170                 2175

acc cta  atg ttg aac ctg gcg  caa atg gaa gac gcg  cac ctg aaa      6579
Thr Leu  Met Leu Asn Leu Ala  Gln Met Glu Asp Ala  His Leu Lys
    2180                 2185                 2190

caa gag  caa cgc gca ctg gaa  gtg gaa cgc acg gtt  tct ctg gcg      6624
Gln Glu  Gln Arg Ala Leu Glu  Val Glu Arg Thr Val  Ser Leu Ala
    2195                 2200                 2205

cag gtg  tac caa tcc tta ggg  gag aaa agc ttt gca  tta aaa gat      6669
Gln Val  Tyr Gln Ser Leu Gly  Glu Lys Ser Phe Ala  Leu Lys Asp
    2210                 2215                 2220

aaa att  gaa gcg ttg cta caa  gga gat aaa gag act  tcc gcc ggt      6714
Lys Ile  Glu Ala Leu Leu Gln  Gly Asp Lys Glu Thr  Ser Ala Gly
    2225                 2230                 2235

aac gac  ggc aat caa ttg aaa  tta acc aac aat acg  cta tcc gcg      6759
Asn Asp  Gly Asn Gln Leu Lys  Leu Thr Asn Asn Thr  Leu Ser Ala
    2240                 2245                 2250

acg cta  acc ctg caa gat ctg  aaa ctc aaa gat gac  tac ccg gaa      6804
Thr Leu  Thr Leu Gln Asp Leu  Lys Leu Lys Asp Asp  Tyr Pro Glu
    2255                 2260                 2265

gag atg  cag tta ggt aaa aca  cgc cgc att aaa caa  att agc gtc      6849
Glu Met  Gln Leu Gly Lys Thr  Arg Arg Ile Lys Gln  Ile Ser Val
    2270                 2275                 2280

tcc tta  ccg gca tta ttg gga  ccg tat caa gat gtt  cag gct gtc      6894
Ser Leu  Pro Ala Leu Leu Gly  Pro Tyr Gln Asp Val  Gln Ala Val
    2285                 2290                 2295

ctg tct  tat ggt ggc gat gcc  acc ggg cta gct aaa  ggt tgt aaa      6939
Leu Ser  Tyr Gly Gly Asp Ala  Thr Gly Leu Ala Lys  Gly Cys Lys
    2300                 2305                 2310

gcc ttg  gcg gtc tcc cac ggc  ctg aat gac aac ggt  cag ttt cag      6984
Ala Leu  Ala Val Ser His Gly  Leu Asn Asp Asn Gly  Gln Phe Gln
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    2315                 2320                 2325

ctc gat  ttt aac gat ggc aaa  ttc ctg ccg ttt gaa  ggg atc gat      7029
Leu Asp  Phe Asn Asp Gly Lys  Phe Leu Pro Phe Glu  Gly Ile Asp
    2330                 2335                 2340

att aat  gac aaa ggg aca ttc  acg cta agt ttc ccc  aat gcc gcc      7074
Ile Asn  Asp Lys Gly Thr Phe  Thr Leu Ser Phe Pro  Asn Ala Ala
    2345                 2350                 2355

agt aaa  caa aaa aat ata tta  cag atg ctg acc gat  att att ctg      7119
Ser Lys  Gln Lys Asn Ile Leu  Gln Met Leu Thr Asp  Ile Ile Leu
    2360                 2365                 2370

cac att  cgt tac act att ctc  gaa taa                               7146
His Ile  Arg Tyr Thr Ile Leu  Glu
    2375                 2380


<210> SEQ ID NO 8
<211> LENGTH: 2381
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 8

Met Asn Ser Tyr Val Lys Glu Ile Pro Asp Val Leu Gln Ser Gln Tyr
1               5                   10                  15

Gly Ile Asn Cys Leu Thr Asp Ile Cys His Tyr Ser Phe Asn Glu Phe
            20                  25                  30

Arg Gln Gln Val Ser Asp His Leu Ser Trp Ser Glu Thr Asn Arg Leu
        35                  40                  45

Tyr Arg Asp Ala Gln Gln Glu Gln Lys Glu Asn Gln Leu Tyr Glu Ala
    50                  55                  60

Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65                  70                  75                  80

Gly Ile Thr Leu Pro His Ala Glu Leu Arg Gly Tyr Asn Ser Glu Phe
                85                  90                  95

Gly Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Ser Val Ser Ser Met
            100                 105                 110

Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
        115                 120                 125

Leu His Ala Ser Asp Ser Val Tyr His Leu Asp Glu Arg Arg Pro Asp
    130                 135                 140

Leu Gln Ser Met Thr Leu Ser Gln Gln Asn Met Asp Thr Glu Leu Ser
145                 150                 155                 160

Thr Leu Ser Leu Ser Asn Glu Ile Leu Leu Lys Gly Ile Lys Ala Asn
                165                 170                 175

Gln Ser Asn Leu Asp Ser Asp Thr Lys Val Met Glu Met Leu Ser Thr
            180                 185                 190

Phe Arg Pro Ser Gly Thr Ile Pro Tyr His Asp Ala Tyr Glu Asn Val
        195                 200                 205

Arg Lys Ala Ile Gln Leu Gln Asp Pro Lys Leu Glu Gln Phe Gln Lys
    210                 215                 220

Ser Pro Ala Val Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile
225                 230                 235                 240

Asn Asn Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile
                245                 250                 255

Thr Glu Ala Asn Ala Glu Ala Ile Tyr Lys Gln Asn Phe Gly Asp Ile
            260                 265                 270

Asp Pro Ala Cys Leu Ala Met Pro Glu Tyr Leu Lys Ser Tyr Tyr Asn
        275                 280                 285
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Phe Ser Asp Glu Glu Leu Ser Gln Phe Ile Arg Lys Tyr Pro Asp Asn
    290                 295                 300

Glu Leu Asn Thr Gln Lys Ile His Leu Leu Lys Ile Asn Lys Ile Ile
305                 310                 315                 320

Leu Leu Ser Gln Ala Val Asn Leu Pro Phe Leu Lys Leu Asp Glu Ile
                325                 330                 335

Ile Pro Glu Gln Asn Ile Thr Pro Thr Val Leu Gly Lys Ile Phe Leu
            340                 345                 350

Val Lys Tyr Tyr Met Gln Lys Tyr Asn Ile Gly Thr Glu Thr Ala Leu
        355                 360                 365

Ile Leu Cys Asn Asp Ser Ile Ser Gln Tyr Ser Tyr Ser Asn Gln Pro
    370                 375                 380

Ser Gln Phe Asp Arg Leu Phe Asn Thr Ser Pro Leu Asn Gly Gln Tyr
385                 390                 395                 400

Phe Val Ile Glu Asp Thr Asn Ile Asp Leu Ser Leu Asn Ser Thr Asp
                405                 410                 415

Asn Trp His Lys Ala Val Leu Lys Arg Ala Phe Asn Val Asp Asp Ile
            420                 425                 430

Ser Leu Tyr Arg Leu Leu His Ile Ala Asn His Asn Asn Thr Asp Gly
        435                 440                 445

Lys Ile Ala Asn Asn Ile Lys Asn Leu Ser Asn Leu Tyr Met Thr Lys
    450                 455                 460

Leu Leu Ala Asp Ile His Gln Leu Thr Ile Asp Glu Leu Tyr Leu Leu
465                 470                 475                 480

Leu Ile Thr Ile Gly Glu Asp Lys Ile Asn Leu Tyr Asp Ile Asp Asp
                485                 490                 495

Lys Glu Leu Glu Lys Leu Ile Asn Arg Leu Asp Thr Leu Ser Asn Trp
            500                 505                 510

Leu His Thr Gln Lys Trp Ser Ile Tyr Gln Leu Phe Leu Met Thr Thr
        515                 520                 525

Thr Asn Tyr Asp Lys Thr Leu Thr Pro Glu Ile Gln Asn Leu Leu Asp
    530                 535                 540

Thr Val Tyr Asn Gly Leu Gln Asn Phe Asp Lys Asn Lys Thr Lys Leu
545                 550                 555                 560

Leu Ala Ala Ile Ala Pro Tyr Ile Ala Ala Thr Leu Gln Leu Pro Ser
                565                 570                 575

Glu Asn Val Ala His Ser Ile Leu Leu Trp Ala Asp Lys Ile Lys Pro
            580                 585                 590

Ser Glu Asn Lys Ile Thr Ala Glu Lys Phe Trp Ile Trp Leu Gln Asn
        595                 600                 605

Arg Asp Thr Thr Glu Leu Ser Lys Pro Pro Glu Met Gln Glu Gln Ile
    610                 615                 620

Ile Gln Tyr Cys His Cys Leu Ala Gln Leu Thr Met Ile Tyr Arg Ser
625                 630                 635                 640

Ser Gly Ile Asn Glu Asn Ala Phe Arg Leu Phe Ile Glu Lys Pro Thr
                645                 650                 655

Ile Phe Gly Ile Pro Asp Glu Pro Asn Lys Ala Thr Pro Ala His Asn
            660                 665                 670

Ala Pro Thr Leu Ile Ile Leu Thr Arg Phe Ala Asn Trp Val Asn Ser
        675                 680                 685

Leu Gly Glu Lys Ala Ser Pro Ile Leu Thr Ala Phe Glu Asn Lys Thr
    690                 695                 700
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Leu Thr Ala Glu Lys Leu Ala Asn Ala Met Asn Leu Asp Ala Asn Leu
705                 710                 715                 720

Leu Glu Gln Ala Ser Ile Gln Ala Gln Asn Tyr Lys Gln Val Thr Lys
                725                 730                 735

Glu Asn Thr Phe Ser Asn Trp Gln Ser Ile Asp Ile Ile Leu Gln Trp
            740                 745                 750

Thr Asn Ile Ala Ser Asn Leu Asn Ile Ser Pro Gln Gly Ile Ser Pro
        755                 760                 765

Leu Ile Ala Leu Asp Tyr Ile Lys Pro Ala Gln Lys Thr Pro Thr Tyr
    770                 775                 780

Ala Gln Trp Glu Asn Ala Ala Ile Ala Leu Thr Ala Gly Leu Asp Thr
785                 790                 795                 800

Gln Gln Thr His Thr Leu His Val Phe Leu Asp Glu Ser Arg Ser Thr
                805                 810                 815

Ala Leu Ser Asn Tyr Tyr Ile Gly Lys Val Ala Asn Arg Ala Ala Ser
            820                 825                 830

Ile Lys Ser Arg Asp Asp Leu Tyr Gln Tyr Leu Leu Ile Asp Asn Gln
        835                 840                 845

Val Ser Ala Glu Ile Lys Thr Thr Arg Ile Ala Glu Ala Ile Ala Ser
    850                 855                 860

Ile Gln Leu Tyr Val Asn Arg Ala Leu Glu Asn Ile Glu Ile His Ala
865                 870                 875                 880

Val Ser Asp Val Ile Thr Arg Gln Phe Phe Ile Asp Trp Asp Lys Tyr
                885                 890                 895

Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Gln Leu Val Tyr Tyr
            900                 905                 910

Pro Glu Asn Tyr Ile Asp Pro Thr Met Arg Ile Gly Gln Thr Lys Met
        915                 920                 925

Met Asp Thr Leu Leu Gln Ser Val Ser Gln Ser Gln Leu Asn Ala Asp
    930                 935                 940

Thr Val Glu Asp Ala Phe Lys Ser Tyr Leu Thr Ser Phe Glu Gln Val
945                 950                 955                 960

Ala Asn Leu Glu Val Ile Ser Ala Tyr His Asp Asn Val Asn Asn Asp
                965                 970                 975

Gln Gly Leu Thr Tyr Phe Ile Gly Asn Ser Lys Thr Glu Val Asn Gln
            980                 985                 990

Tyr Tyr Trp Arg Ser Val Asp His  Ser Lys Phe Asn Asp  Gly Lys Phe
        995                 1000                 1005

Ala Ala  Asn Ala Trp Ser Glu  Trp His Lys Ile Asp  Cys Ala Ile
    1010                 1015                 1020

Asn Pro  Tyr Gln Ser Thr Ile  Arg Pro Val Ile Tyr  Lys Ser Arg
    1025                 1030                 1035

Leu Tyr  Leu Ile Trp Leu Glu  Gln Lys Glu Thr Ala  Lys Gln Lys
    1040                 1045                 1050

Glu Asp  Asn Lys Val Thr Thr  Asp Tyr His Tyr Glu  Leu Lys Leu
    1055                 1060                 1065

Ala His  Ile Arg Tyr Asp Gly  Thr Trp Asn Val Pro  Ile Thr Phe
    1070                 1075                 1080

Asp Val  Asp Glu Lys Ile Leu  Ala Leu Glu Leu Thr  Lys Ser Gln
    1085                 1090                 1095

Ala Pro  Gly Leu Tyr Cys Ala  Gly Tyr Gln Gly Glu  Asp Thr Leu
    1100                 1105                 1110

Leu Ile  Met Phe Tyr Arg Lys  Lys Glu Lys Leu Asp  Asp Tyr Lys
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    1115                1120                1125

Thr Ala  Pro Met Gln Gly Phe  Tyr Ile Phe Ser Asp  Met Ser Ser
    1130                1135                1140

Lys Asp  Met Thr Asn Glu Gln  Cys Asn Ser Tyr Arg  Asp Asn Gly
    1145                1150                1155

Tyr Thr  His Phe Asp Thr Asn  Ser Asp Thr Asn Ser  Val Ile Arg
    1160                1165                1170

Ile Asn  Asn Arg Tyr Ala Glu  Asp Tyr Glu Ile Pro  Ser Leu Ile
    1175                1180                1185

Asn His  Ser Asn Ser His Asp  Trp Gly Glu Tyr Asn  Leu Ser Gln
    1190                1195                1200

Val Tyr  Gly Gly Asn Ile Val  Ile Asn Tyr Lys Val  Thr Ser Asn
    1205                1210                1215

Asp Leu  Lys Ile Tyr Ile Ser  Pro Lys Leu Arg Ile  Ile His Asp
    1220                1225                1230

Gly Lys  Glu Gly Arg Glu Arg  Ile Gln Ser Asn Leu  Ile Lys Lys
    1235                1240                1245

Tyr Gly  Lys Leu Gly Asp Lys  Phe Ile Ile Tyr Thr  Ser Leu Gly
    1250                1255                1260

Ile Asn  Pro Asn Asn Ser Ser  Asn Arg Phe Met Phe  Tyr Pro Val
    1265                1270                1275

Tyr Gln  Tyr Asn Gly Asn Thr  Ser Gly Leu Ala Gln  Gly Arg Leu
    1280                1285                1290

Leu Phe  His Arg Asp Thr Ser  Tyr Ser Ser Lys Val  Ala Ala Trp
    1295                1300                1305

Ile Pro  Gly Ala Gly Arg Ser  Leu Ile Asn Glu Asn  Ala Asn Ile
    1310                1315                1320

Gly Asp  Asp Cys Ala Glu Asp  Ser Val Asn Lys Pro  Asp Asp Leu
    1325                1330                1335

Lys Gln  Tyr Ile Tyr Met Thr  Asp Ser Lys Gly Thr  Ala Thr Asp
    1340                1345                1350

Val Ser  Gly Pro Val Asp Ile  Asn Thr Ala Ile Ser  Ser Glu Lys
    1355                1360                1365

Val Gln  Ile Thr Ile Lys Ala  Gly Lys Glu Tyr Ser  Leu Thr Ala
    1370                1375                1380

Asn Lys  Asp Val Ser Val Gln  Pro Ser Pro Ser Phe  Glu Glu Met
    1385                1390                1395

Cys Tyr  Gln Phe Asn Ala Leu  Glu Ile Asp Gly Ser  Asn Leu Asn
    1400                1405                1410

Phe Thr  Asn Asn Ser Ala Ser  Ile Asp Val Thr Phe  Thr Ala Leu
    1415                1420                1425

Ala Asp  Asp Gly Arg Lys Leu  Gly Tyr Glu Ile Phe  Asn Ile Pro
    1430                1435                1440

Val Ile  Gln Lys Val Lys Thr  Asp Asn Ala Leu Thr  Leu Phe His
    1445                1450                1455

Asp Glu  Asn Gly Ala Gln Tyr  Met Gln Trp Gly Ala  Tyr Arg Ile
    1460                1465                1470

Arg Leu  Asn Thr Leu Phe Ala  Arg Gln Leu Val Glu  Arg Ala Asn
    1475                1480                1485

Thr Gly  Ile Asp Thr Ile Leu  Ser Met Glu Thr Gln  Asn Ile Gln
    1490                1495                1500

Glu Pro  Met Met Gly Ile Gly  Ala Tyr Ile Glu Leu  Ile Leu Asp
    1505                1510                1515
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Lys Tyr  Asn Pro Asp Ile His  Gly Thr Asn Lys Ser  Phe Lys Ile
    1520                 1525                 1530

Ile Tyr  Gly Asp Ile Phe Lys  Ala Gly Asp His Phe  Pro Ile Tyr
    1535                 1540                 1545

Gln Gly  Ala Leu Ser Asp Ile  Thr Gln Thr Thr Val  Lys Leu Phe
    1550                 1555                 1560

Leu Pro  Arg Val Asp Asn Ala  Tyr Gly Asn Lys Asn  Asn Leu Tyr
    1565                 1570                 1575

Val Tyr  Ala Ala Tyr Gln Lys  Val Glu Thr Asn Phe  Ile Arg Phe
    1580                 1585                 1590

Val Lys  Glu Asp Asn Asn Lys  Pro Ala Thr Phe Asp  Thr Thr Tyr
    1595                 1600                 1605

Lys Asn  Gly Thr Phe Pro Gly  Leu Ala Ser Ala Arg  Val Ile Gln
    1610                 1615                 1620

Thr Val  Ser Glu Pro Met Asp  Phe Ser Gly Ala Asn  Ser Leu Tyr
    1625                 1630                 1635

Phe Trp  Glu Leu Phe Tyr Tyr  Thr Pro Met Met Val  Ala Gln Arg
    1640                 1645                 1650

Leu Leu  His Glu Gln Asn Phe  Asp Glu Ala Asn Arg  Trp Leu Lys
    1655                 1660                 1665

Tyr Val  Trp Ser Pro Ser Gly  Tyr Ile Val Arg Gly  Gln Ile Lys
    1670                 1675                 1680

Asn Tyr  His Trp Asn Val Arg  Pro Leu Leu Glu Asn  Thr Ser Trp
    1685                 1690                 1695

Asn Ser  Asp Pro Leu Asp Ser  Val Asp Pro Asp Ala  Val Ala Gln
    1700                 1705                 1710

His Asp  Pro Met His Tyr Lys  Val Ala Thr Phe Met  Arg Thr Leu
    1715                 1720                 1725

Asp Leu  Leu Met Ala Arg Gly  Asp His Ala Tyr Arg  Gln Leu Glu
    1730                 1735                 1740

Arg Asp  Thr Leu Asn Glu Ala  Lys Met Trp Tyr Met  Gln Ala Leu
    1745                 1750                 1755

His Leu  Leu Gly Asn Lys Pro  Tyr Leu Pro Leu Ser  Ser Val Trp
    1760                 1765                 1770

Asn Asp  Pro Arg Leu Asp Asn  Ala Ala Ala Thr Thr  Thr Gln Lys
    1775                 1780                 1785

Ala His  Ala Tyr Ala Ile Thr  Ser Leu Arg Gln Gly  Thr Gln Thr
    1790                 1795                 1800

Pro Ala  Leu Leu Leu Arg Ser  Ala Asn Thr Leu Thr  Asp Leu Phe
    1805                 1810                 1815

Leu Pro  Gln Ile Asn Asp Val  Met Leu Ser Tyr Trp  Asn Lys Leu
    1820                 1825                 1830

Glu Leu  Arg Leu Tyr Asn Leu  Arg His Asn Leu Ser  Ile Asp Gly
    1835                 1840                 1845

Gln Pro  Leu His Leu Pro Ile  Tyr Ala Thr Pro Ala  Asp Pro Lys
    1850                 1855                 1860

Ala Leu  Leu Ser Ala Ala Val  Ala Thr Ser Gln Gly  Gly Gly Lys
    1865                 1870                 1875

Leu Pro  Glu Ser Phe Ile Ser  Leu Trp Arg Phe Pro  His Met Leu
    1880                 1885                 1890

Glu Asn  Ala Arg Ser Met Val  Thr Gln Leu Ile Gln  Phe Gly Ser
    1895                 1900                 1905
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Thr Leu  Gln Asn Ile Ile Glu  Arg Gln Asp Ala Glu  Ser Leu Asn
    1910                 1915                 1920

Ala Leu  Leu Gln Asn Gln Ala  Lys Glu Leu Ile Leu  Thr Thr Leu
    1925                 1930                 1935

Ser Ile  Gln Asp Lys Thr Ile  Glu Glu Ile Asp Ala  Glu Lys Thr
    1940                 1945                 1950

Val Leu  Glu Lys Ser Lys Ala  Gly Ala Lys Ser Arg  Phe Asp Asn
    1955                 1960                 1965

Tyr Ser  Lys Leu Tyr Asp Glu  Asp Val Asn Ala Gly  Glu Arg Gln
    1970                 1975                 1980

Ala Leu  Asp Met Arg Ile Ala  Ser Gln Ser Ile Thr  Ser Gly Leu
    1985                 1990                 1995

Lys Gly  Leu His Met Ala Ala  Ala Ala Leu Glu Met  Val Pro Asn
    2000                 2005                 2010

Ile Tyr  Gly Phe Ala Val Gly  Gly Thr Arg Tyr Gly  Ala Ile Ala
    2015                 2020                 2025

Asn Ala  Ile Ala Ile Gly Gly  Gly Ile Ala Ala Glu  Gly Leu Leu
    2030                 2035                 2040

Ile Glu  Ala Glu Lys Val Ser  Gln Ser Glu Ile Trp  Arg Arg Arg
    2045                 2050                 2055

Arg Gln  Glu Trp Glu Ile Gln  Arg Asn Asn Ala Glu  Ala Glu Met
    2060                 2065                 2070

Lys Gln  Ile Asp Ala Gln Leu  Lys Ser Leu Thr Val  Arg Arg Glu
    2075                 2080                 2085

Ala Ala  Val Leu Gln Lys Thr  Gly Leu Lys Thr Gln  Gln Glu Gln
    2090                 2095                 2100

Thr Gln  Ala Gln Leu Ala Phe  Leu Gln Arg Lys Phe  Ser Asn Gln
    2105                 2110                 2115

Ala Leu  Tyr Asn Trp Leu Arg  Gly Arg Leu Ala Ala  Ile Tyr Phe
    2120                 2125                 2130

Gln Phe  Tyr Asp Leu Val Val  Ala Arg Cys Leu Met  Ala Glu Gln
    2135                 2140                 2145

Ala Tyr  Arg Trp Glu Thr Asn  Asp Ser Ser Ala Arg  Phe Ile Lys
    2150                 2155                 2160

Pro Gly  Ala Trp Gln Gly Thr  Tyr Ala Gly Leu Leu  Ala Gly Glu
    2165                 2170                 2175

Thr Leu  Met Leu Asn Leu Ala  Gln Met Glu Asp Ala  His Leu Lys
    2180                 2185                 2190

Gln Glu  Gln Arg Ala Leu Glu  Val Glu Arg Thr Val  Ser Leu Ala
    2195                 2200                 2205

Gln Val  Tyr Gln Ser Leu Gly  Glu Lys Ser Phe Ala  Leu Lys Asp
    2210                 2215                 2220

Lys Ile  Glu Ala Leu Leu Gln  Gly Asp Lys Glu Thr  Ser Ala Gly
    2225                 2230                 2235

Asn Asp  Gly Asn Gln Leu Lys  Leu Thr Asn Asn Thr  Leu Ser Ala
    2240                 2245                 2250

Thr Leu  Thr Leu Gln Asp Leu  Lys Leu Lys Asp Asp  Tyr Pro Glu
    2255                 2260                 2265

Glu Met  Gln Leu Gly Lys Thr  Arg Arg Ile Lys Gln  Ile Ser Val
    2270                 2275                 2280

Ser Leu  Pro Ala Leu Leu Gly  Pro Tyr Gln Asp Val  Gln Ala Val
    2285                 2290                 2295

Leu Ser  Tyr Gly Gly Asp Ala  Thr Gly Leu Ala Lys  Gly Cys Lys
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    2300                 2305                 2310

Ala Leu  Ala Val Ser His Gly  Leu Asn Asp Asn Gly  Gln Phe Gln
    2315                 2320                 2325

Leu Asp  Phe Asn Asp Gly Lys  Phe Leu Pro Phe Glu  Gly Ile Asp
    2330                 2335                 2340

Ile Asn  Asp Lys Gly Thr Phe  Thr Leu Ser Phe Pro  Asn Ala Ala
    2345                 2350                 2355

Ser Lys  Gln Lys Asn Ile Leu  Gln Met Leu Thr Asp  Ile Ile Leu
    2360                 2365                 2370

His Ile  Arg Tyr Thr Ile Leu  Glu
    2375                 2380


<210> SEQ ID NO 9
<211> LENGTH: 4425
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
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<222> LOCATION: (1)..(4422)

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atg caa aat tca caa gat ttt agt att acg gaa ctg tca ctg ccc aaa       48
Met Gln Asn Ser Gln Asp Phe Ser Ile Thr Glu Leu Ser Leu Pro Lys
1               5                   10                  15

ggg ggg ggc gct atc acg gga atg ggt gaa gca tta acc ccc act gga       96
Gly Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Thr Gly
            20                  25                  30

ccg gat ggt atg gcc gcg cta tct cta cca ttg cct att tct gcc ggg      144
Pro Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly
        35                  40                  45

cgc ggt tat gct ccc gca ttc act ctg aat tac aac agc ggc gcc ggt      192
Arg Gly Tyr Ala Pro Ala Phe Thr Leu Asn Tyr Asn Ser Gly Ala Gly
    50                  55                  60

aac agt cca ttt ggt ctg ggt tgg gat tgc aac gtt atg act atc cgc      240
Asn Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg
65                  70                  75                  80

cgc cgc acc cat ttt ggc gtc ccc cat tat gac gaa acc gat acc ttt      288
Arg Arg Thr His Phe Gly Val Pro His Tyr Asp Glu Thr Asp Thr Phe
                85                  90                  95

ttg ggg cca gaa ggc gaa gtg ctg gtg gta gcg gat caa cct cgc gac      336
Leu Gly Pro Glu Gly Glu Val Leu Val Val Ala Asp Gln Pro Arg Asp
            100                 105                 110

gaa tcc aca tta cag ggt atc aat tta ggc gcc acc ttt acc gtt acc      384
Glu Ser Thr Leu Gln Gly Ile Asn Leu Gly Ala Thr Phe Thr Val Thr
        115                 120                 125

ggc tac cgt tcc cgt ctg gaa agc cat ttc agc cga ttg gaa tat tgg      432
Gly Tyr Arg Ser Arg Leu Glu Ser His Phe Ser Arg Leu Glu Tyr Trp
    130                 135                 140

caa ccc aaa aca aca ggt aaa aca gat ttt tgg ttg ata tat agc cca      480
Gln Pro Lys Thr Thr Gly Lys Thr Asp Phe Trp Leu Ile Tyr Ser Pro
145                 150                 155                 160

gat ggg cag gtg cat cta ctg ggt aaa tca ccg caa gcg cgg atc agc      528
Asp Gly Gln Val His Leu Leu Gly Lys Ser Pro Gln Ala Arg Ile Ser
                165                 170                 175

aac cca tcc caa acg aca caa aca gca caa tgg ctg ctg gaa gcc tct      576
Asn Pro Ser Gln Thr Thr Gln Thr Ala Gln Trp Leu Leu Glu Ala Ser
            180                 185                 190

gta tca tca cgt ggc gaa caa att tat tat caa tat cgc gcc gaa gat      624
Val Ser Ser Arg Gly Glu Gln Ile Tyr Tyr Gln Tyr Arg Ala Glu Asp
        195                 200                 205
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gac aca ggt tgc gaa gca gat gaa att acg cac cat tta cag gct aca      672
Asp Thr Gly Cys Glu Ala Asp Glu Ile Thr His His Leu Gln Ala Thr
    210                 215                 220

gcg caa cgt tat tta cac atc gtg tat tac ggc aac cgt aca gcc agc      720
Ala Gln Arg Tyr Leu His Ile Val Tyr Tyr Gly Asn Arg Thr Ala Ser
225                 230                 235                 240

gaa aca tta ccc ggt ctg gat ggc agc gcc cca tca caa gca gac tgg      768
Glu Thr Leu Pro Gly Leu Asp Gly Ser Ala Pro Ser Gln Ala Asp Trp
                245                 250                 255

ttg ttc tat ctg gta ttt gat tac ggc gaa cgc agt aac aac ctg aaa      816
Leu Phe Tyr Leu Val Phe Asp Tyr Gly Glu Arg Ser Asn Asn Leu Lys
            260                 265                 270

acg cca cca gca ttt tcg act aca ggt agc tgg ctt tgc cgt cag gac      864
Thr Pro Pro Ala Phe Ser Thr Thr Gly Ser Trp Leu Cys Arg Gln Asp
        275                 280                 285

cgt ttt tcc cgt tat gaa tat ggc ttt gag att cgt acc cgc cgc tta      912
Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Glu Ile Arg Thr Arg Arg Leu
    290                 295                 300

tgc cgt cag gta ttg atg tac cat cac ctg caa gca ctg gat agt aag      960
Cys Arg Gln Val Leu Met Tyr His His Leu Gln Ala Leu Asp Ser Lys
305                 310                 315                 320

ata aca gaa cac aac gga cca acg ctg gtt tca cgc ctg ata ctc aat     1008
Ile Thr Glu His Asn Gly Pro Thr Leu Val Ser Arg Leu Ile Leu Asn
                325                 330                 335

tac gac gaa agc gcg ata gcc agc acg cta gta ttc gtt cgc cga gtg     1056
Tyr Asp Glu Ser Ala Ile Ala Ser Thr Leu Val Phe Val Arg Arg Val
            340                 345                 350

gga cac gag caa gat ggt aat gtc gtc acc ctg ccg cca tta gaa ttg     1104
Gly His Glu Gln Asp Gly Asn Val Val Thr Leu Pro Pro Leu Glu Leu
        355                 360                 365

gca tat cag gat ttt tca ccg cga cat cac gct cac tgg caa cca atg     1152
Ala Tyr Gln Asp Phe Ser Pro Arg His His Ala His Trp Gln Pro Met
    370                 375                 380

gat gta ctg gca aac ttc aat gcc att cag cgc tgg cag cta gtc gat     1200
Asp Val Leu Ala Asn Phe Asn Ala Ile Gln Arg Trp Gln Leu Val Asp
385                 390                 395                 400

cta aaa ggc gaa gga tta ccc ggc ctg tta tat cag gat aaa ggc gct     1248
Leu Lys Gly Glu Gly Leu Pro Gly Leu Leu Tyr Gln Asp Lys Gly Ala
                405                 410                 415

tgg tgg tac cgc tcc gca cag cgt ctg ggc gaa att ggc tca gat gcc     1296
Trp Trp Tyr Arg Ser Ala Gln Arg Leu Gly Glu Ile Gly Ser Asp Ala
            420                 425                 430

gtc act tgg gaa aag atg caa cct tta tcg gtt att cct tct ttg caa     1344
Val Thr Trp Glu Lys Met Gln Pro Leu Ser Val Ile Pro Ser Leu Gln
        435                 440                 445

agt aat gcc tcg ttg gtg gat atc aat gga gac ggc caa ctt gac tgg     1392
Ser Asn Ala Ser Leu Val Asp Ile Asn Gly Asp Gly Gln Leu Asp Trp
    450                 455                 460

gtt atc acc gga ccg gga tta cgg gga tat cat agt caa cgc ccg gat     1440
Val Ile Thr Gly Pro Gly Leu Arg Gly Tyr His Ser Gln Arg Pro Asp
465                 470                 475                 480

ggc agt tgg aca cgt ttt acc cca ctc aac gct ctg ccg gtg gaa tac     1488
Gly Ser Trp Thr Arg Phe Thr Pro Leu Asn Ala Leu Pro Val Glu Tyr
                485                 490                 495

acc cat cca cgc gcg caa ctc gca gat tta atg gga gcc ggg cta tcc     1536
Thr His Pro Arg Ala Gln Leu Ala Asp Leu Met Gly Ala Gly Leu Ser
            500                 505                 510

gat ttg gtg ctg atc ggc cct aag agc gtg cgt tta tat gcc aat acc     1584
Asp Leu Val Leu Ile Gly Pro Lys Ser Val Arg Leu Tyr Ala Asn Thr
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        515                 520                 525

cgc gac ggc ttt gcc aaa gga aaa gat gtg gtg caa tcc ggt gat atc     1632
Arg Asp Gly Phe Ala Lys Gly Lys Asp Val Val Gln Ser Gly Asp Ile
    530                 535                 540

aca ctg ccg gtg ccg ggc gcc gat cca cgt aag ttg gtg gcg ttt agt     1680
Thr Leu Pro Val Pro Gly Ala Asp Pro Arg Lys Leu Val Ala Phe Ser
545                 550                 555                 560

gat gta ttg ggt tca ggt caa gcc cat ctg gtt gaa gta agc gcg act     1728
Asp Val Leu Gly Ser Gly Gln Ala His Leu Val Glu Val Ser Ala Thr
                565                 570                 575

aaa gtc acc tgc tgg cct aat ctg ggg cgc gga cgt ttt ggt caa ccc     1776
Lys Val Thr Cys Trp Pro Asn Leu Gly Arg Gly Arg Phe Gly Gln Pro
            580                 585                 590

att acc tta ccg gga ttc agc cag cca gca acc gag ttt aac ccg gct     1824
Ile Thr Leu Pro Gly Phe Ser Gln Pro Ala Thr Glu Phe Asn Pro Ala
        595                 600                 605

caa gtt tat ctg gcc gat ctg gat ggc agc ggt cca acg gat ctg att     1872
Gln Val Tyr Leu Ala Asp Leu Asp Gly Ser Gly Pro Thr Asp Leu Ile
    610                 615                 620

tat gtt cat aca aac cgt ctg gat atc ttc ctg aac aaa agt ggc aat     1920
Tyr Val His Thr Asn Arg Leu Asp Ile Phe Leu Asn Lys Ser Gly Asn
625                 630                 635                 640

ggc ttt gct gaa cca gtg aca tta cgc ttc ccg gaa ggt ctg cgt ttt     1968
Gly Phe Ala Glu Pro Val Thr Leu Arg Phe Pro Glu Gly Leu Arg Phe
                645                 650                 655

gat cat acc tgt cag tta caa atg gcc gat gta caa gga tta ggc gtc     2016
Asp His Thr Cys Gln Leu Gln Met Ala Asp Val Gln Gly Leu Gly Val
            660                 665                 670

gcc agc ctg ata ctg agc gtg ccg cat atg tct ccc cat cac tgg cgc     2064
Ala Ser Leu Ile Leu Ser Val Pro His Met Ser Pro His His Trp Arg
        675                 680                 685

tgc gat ctg acc aac atg aag ccg tgg tta ctc aat gaa atg aac aac     2112
Cys Asp Leu Thr Asn Met Lys Pro Trp Leu Leu Asn Glu Met Asn Asn
    690                 695                 700

aat atg ggg gtc cat cac acc ttg cgt tac cgc agt tcc tcc caa ttc     2160
Asn Met Gly Val His His Thr Leu Arg Tyr Arg Ser Ser Ser Gln Phe
705                 710                 715                 720

tgg ctg gat gaa aaa gcc gcg gcg ctg act acc gga caa aca ccg gtt     2208
Trp Leu Asp Glu Lys Ala Ala Ala Leu Thr Thr Gly Gln Thr Pro Val
                725                 730                 735

tgc tat ctc ccc ttc ccg atc cac acc cta tgg caa acg gaa aca gaa     2256
Cys Tyr Leu Pro Phe Pro Ile His Thr Leu Trp Gln Thr Glu Thr Glu
            740                 745                 750

gat gaa atc agc ggc aac aaa tta gtc aca aca ctt cgt tat gct cgt     2304
Asp Glu Ile Ser Gly Asn Lys Leu Val Thr Thr Leu Arg Tyr Ala Arg
        755                 760                 765

ggc gca tgg gac gga cgc gag cgg gaa ttt cgc gga ttt ggt tat gta     2352
Gly Ala Trp Asp Gly Arg Glu Arg Glu Phe Arg Gly Phe Gly Tyr Val
    770                 775                 780

gag cag aca gac agc cat caa ctg gct caa ggc aac gcg cca gaa cgt     2400
Glu Gln Thr Asp Ser His Gln Leu Ala Gln Gly Asn Ala Pro Glu Arg
785                 790                 795                 800

acg cca ccg gcg ctg acc aaa aac tgg tat gcc acc gga ctg ccg gtg     2448
Thr Pro Pro Ala Leu Thr Lys Asn Trp Tyr Ala Thr Gly Leu Pro Val
                805                 810                 815

ata gat aac gca tta tca acc gag tat tgg cgt gat gat cag gct ttt     2496
Ile Asp Asn Ala Leu Ser Thr Glu Tyr Trp Arg Asp Asp Gln Ala Phe
            820                 825                 830

gcc ggt ttc tca ccg cgc ttt acg act tgg caa gat aac aaa gat gtc     2544
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Ala Gly Phe Ser Pro Arg Phe Thr Thr Trp Gln Asp Asn Lys Asp Val
        835                 840                 845

ccg tta aca ccg gaa gat gat aac agt cgt tac tgg ttc aac cgc gcg     2592
Pro Leu Thr Pro Glu Asp Asp Asn Ser Arg Tyr Trp Phe Asn Arg Ala
    850                 855                 860

ttg aaa ggt caa ctg cta cgt agt gaa ctg tac gga ttg gac gat agt     2640
Leu Lys Gly Gln Leu Leu Arg Ser Glu Leu Tyr Gly Leu Asp Asp Ser
865                 870                 875                 880

aca aat aaa cac gtt ccc tat act gtc act gaa ttt cgt tca cag gta     2688
Thr Asn Lys His Val Pro Tyr Thr Val Thr Glu Phe Arg Ser Gln Val
                885                 890                 895

cgt cga tta cag cat acc gac agc cga tac cct gta ctt tgg tca tct     2736
Arg Arg Leu Gln His Thr Asp Ser Arg Tyr Pro Val Leu Trp Ser Ser
            900                 905                 910

gta gtt gaa agc cgc aac tat cac tac gaa cgt atc gcc agc gac ccg     2784
Val Val Glu Ser Arg Asn Tyr His Tyr Glu Arg Ile Ala Ser Asp Pro
        915                 920                 925

caa tgc agt caa aat att acg cta tcc agt gat cga ttt ggt cag ccg     2832
Gln Cys Ser Gln Asn Ile Thr Leu Ser Ser Asp Arg Phe Gly Gln Pro
    930                 935                 940

cta aaa cag ctt tcg gta cag tac ccg cgc cgc cag cag cca gca atc     2880
Leu Lys Gln Leu Ser Val Gln Tyr Pro Arg Arg Gln Gln Pro Ala Ile
945                 950                 955                 960

aat ctg tat cct gat aca ttg cct gat aag ttg tta gcc aac agc tat     2928
Asn Leu Tyr Pro Asp Thr Leu Pro Asp Lys Leu Leu Ala Asn Ser Tyr
                965                 970                 975

gat gac caa caa cgc caa tta cgg ctc acc tat caa caa tcc agt tgg     2976
Asp Asp Gln Gln Arg Gln Leu Arg Leu Thr Tyr Gln Gln Ser Ser Trp
            980                 985                 990

cat cac ctg acc aac aat acc gtt  cga gta ttg gga tta  ccg gat agt   3024
His His Leu Thr Asn Asn Thr Val  Arg Val Leu Gly Leu  Pro Asp Ser
        995                 1000                 1005

acc cgc  agt gat atc ttt act  tat ggc gct gaa aat  gtg cct gct      3069
Thr Arg  Ser Asp Ile Phe Thr  Tyr Gly Ala Glu Asn  Val Pro Ala
    1010                 1015                 1020

ggt ggt  tta aat ctg gaa ctt  ctg agt gat aaa aat  agc ctg atc      3114
Gly Gly  Leu Asn Leu Glu Leu  Leu Ser Asp Lys Asn  Ser Leu Ile
    1025                 1030                 1035

gcg gac  gat aaa cca cgt gaa  tac ctc ggt cag caa  aaa acc gct      3159
Ala Asp  Asp Lys Pro Arg Glu  Tyr Leu Gly Gln Gln  Lys Thr Ala
    1040                 1045                 1050

tat acc  gat gga caa aat aca  acg ccg ttg caa aca  cca aca cgg      3204
Tyr Thr  Asp Gly Gln Asn Thr  Thr Pro Leu Gln Thr  Pro Thr Arg
    1055                 1060                 1065

caa gcc  ctg att gcc ttt acc  gaa aca acg gta ttc  aac cag tcc      3249
Gln Ala  Leu Ile Ala Phe Thr  Glu Thr Thr Val Phe  Asn Gln Ser
    1070                 1075                 1080

aca tta  tca gcg ttt aac gga  agc atc ccg tcc gat  aaa tta tca      3294
Thr Leu  Ser Ala Phe Asn Gly  Ser Ile Pro Ser Asp  Lys Leu Ser
    1085                 1090                 1095

acg acg  ctg gag caa gct gga  tat cag caa aca aat  tat cta ttc      3339
Thr Thr  Leu Glu Gln Ala Gly  Tyr Gln Gln Thr Asn  Tyr Leu Phe
    1100                 1105                 1110

cct cgc  act gga gaa gat aaa  gtt tgg gta gcc cat  cac ggc tat      3384
Pro Arg  Thr Gly Glu Asp Lys  Val Trp Val Ala His  His Gly Tyr
    1115                 1120                 1125

acc gat  tat ggt aca gcg gca  cag ttc tgg cgc ccg  caa aaa cag      3429
Thr Asp  Tyr Gly Thr Ala Ala  Gln Phe Trp Arg Pro  Gln Lys Gln
    1130                 1135                 1140
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agc aac  acc caa ctc acc ggt  aaa atc acc ctc atc  tgg gat gca      3474
Ser Asn  Thr Gln Leu Thr Gly  Lys Ile Thr Leu Ile  Trp Asp Ala
    1145                 1150                 1155

aac tat  tgc gtt gtg gta caa  acc cgg gat gct gct  gga ctg aca      3519
Asn Tyr  Cys Val Val Val Gln  Thr Arg Asp Ala Ala  Gly Leu Thr
    1160                 1165                 1170

acc tca  gcc aaa tat gac tgg  cgt ttt ctg acc ccg  gtg caa ctc      3564
Thr Ser  Ala Lys Tyr Asp Trp  Arg Phe Leu Thr Pro  Val Gln Leu
    1175                 1180                 1185

acc gat  atc aat gac aat cag  cac ctt atc aca ctg  gat gca ttg      3609
Thr Asp  Ile Asn Asp Asn Gln  His Leu Ile Thr Leu  Asp Ala Leu
    1190                 1195                 1200

ggc cga  cca atc aca ttg cgc  ttt tgg gga act gaa  aac ggc aag      3654
Gly Arg  Pro Ile Thr Leu Arg  Phe Trp Gly Thr Glu  Asn Gly Lys
    1205                 1210                 1215

atg aca  ggt tat tcc tca ccg  gaa aaa gca tca ttt  tct cca cca      3699
Met Thr  Gly Tyr Ser Ser Pro  Glu Lys Ala Ser Phe  Ser Pro Pro
    1220                 1225                 1230

tcc gat  gtt aat gcc gct att  gag tta aaa aaa ccg  ctc cct gta      3744
Ser Asp  Val Asn Ala Ala Ile  Glu Leu Lys Lys Pro  Leu Pro Val
    1235                 1240                 1245

gca cag  tgt cag gtc tac gca  cca gaa agc tgg atg  cca gta tta      3789
Ala Gln  Cys Gln Val Tyr Ala  Pro Glu Ser Trp Met  Pro Val Leu
    1250                 1255                 1260

agt cag  aaa acc ttc aat cga  ctg gca gaa caa gat  tgg caa aag      3834
Ser Gln  Lys Thr Phe Asn Arg  Leu Ala Glu Gln Asp  Trp Gln Lys
    1265                 1270                 1275

tta tat  aac gcc cga atc atc  acc gaa gat gga cgt  atc tgc aca      3879
Leu Tyr  Asn Ala Arg Ile Ile  Thr Glu Asp Gly Arg  Ile Cys Thr
    1280                 1285                 1290

ctg gct  tat cgc cgc tgg gta  caa agc caa aag gca  atc cct caa      3924
Leu Ala  Tyr Arg Arg Trp Val  Gln Ser Gln Lys Ala  Ile Pro Gln
    1295                 1300                 1305

ctc att  agc ctg tta aac aac  gga ccc cgt tta cct  cct cac agc      3969
Leu Ile  Ser Leu Leu Asn Asn  Gly Pro Arg Leu Pro  Pro His Ser
    1310                 1315                 1320

ctg aca  ttg acg acg gat cgt  tat gat cac gat cct  gag caa cag      4014
Leu Thr  Leu Thr Thr Asp Arg  Tyr Asp His Asp Pro  Glu Gln Gln
    1325                 1330                 1335

atc cgt  caa cag gtg gta ttc  agt gat ggc ttt ggc  cgc ttg ctg      4059
Ile Arg  Gln Gln Val Val Phe  Ser Asp Gly Phe Gly  Arg Leu Leu
    1340                 1345                 1350

caa gcc  gct gcc cga cat gag  gca ggc atg gcc cgg  caa cgc aat      4104
Gln Ala  Ala Ala Arg His Glu  Ala Gly Met Ala Arg  Gln Arg Asn
    1355                 1360                 1365

gaa gac  ggc tct ttg att ata  aat gtc cag cat act  gag aac cgt      4149
Glu Asp  Gly Ser Leu Ile Ile  Asn Val Gln His Thr  Glu Asn Arg
    1370                 1375                 1380

tgg gca  gtg act gga cga acg  gaa tat gac aat aag  ggg caa ccg      4194
Trp Ala  Val Thr Gly Arg Thr  Glu Tyr Asp Asn Lys  Gly Gln Pro
    1385                 1390                 1395

ata cgt  acc tat cag ccc tat  ttc ctc aat gac tgg  cga tac gtc      4239
Ile Arg  Thr Tyr Gln Pro Tyr  Phe Leu Asn Asp Trp  Arg Tyr Val
    1400                 1405                 1410

agc aat  gat agt gcc cgg cag  gaa aaa gaa gct tat  gca gat acc      4284
Ser Asn  Asp Ser Ala Arg Gln  Glu Lys Glu Ala Tyr  Ala Asp Thr
    1415                 1420                 1425

cat gtc  tat gat ccc ata ggt  cga gaa atc aag gtt  atc acc gca      4329
His Val  Tyr Asp Pro Ile Gly  Arg Glu Ile Lys Val  Ile Thr Ala
    1430                 1435                 1440
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aaa ggt  tgg ttc cgt cga acc  ttg ttc act ccc tgg  ttt act gtc      4374
Lys Gly  Trp Phe Arg Arg Thr  Leu Phe Thr Pro Trp  Phe Thr Val
    1445                 1450                 1455

aat gaa  gat gaa aat gac aca  gcc gct gag gtg aag  aag gta aag      4419
Asn Glu  Asp Glu Asn Asp Thr  Ala Ala Glu Val Lys  Lys Val Lys
    1460                 1465                 1470

atg taa                                                             4425
Met


<210> SEQ ID NO 10
<211> LENGTH: 1474
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 10

Met Gln Asn Ser Gln Asp Phe Ser Ile Thr Glu Leu Ser Leu Pro Lys
1               5                   10                  15

Gly Gly Gly Ala Ile Thr Gly Met Gly Glu Ala Leu Thr Pro Thr Gly
            20                  25                  30

Pro Asp Gly Met Ala Ala Leu Ser Leu Pro Leu Pro Ile Ser Ala Gly
        35                  40                  45

Arg Gly Tyr Ala Pro Ala Phe Thr Leu Asn Tyr Asn Ser Gly Ala Gly
    50                  55                  60

Asn Ser Pro Phe Gly Leu Gly Trp Asp Cys Asn Val Met Thr Ile Arg
65                  70                  75                  80

Arg Arg Thr His Phe Gly Val Pro His Tyr Asp Glu Thr Asp Thr Phe
                85                  90                  95

Leu Gly Pro Glu Gly Glu Val Leu Val Val Ala Asp Gln Pro Arg Asp
            100                 105                 110

Glu Ser Thr Leu Gln Gly Ile Asn Leu Gly Ala Thr Phe Thr Val Thr
        115                 120                 125

Gly Tyr Arg Ser Arg Leu Glu Ser His Phe Ser Arg Leu Glu Tyr Trp
    130                 135                 140

Gln Pro Lys Thr Thr Gly Lys Thr Asp Phe Trp Leu Ile Tyr Ser Pro
145                 150                 155                 160

Asp Gly Gln Val His Leu Leu Gly Lys Ser Pro Gln Ala Arg Ile Ser
                165                 170                 175

Asn Pro Ser Gln Thr Thr Gln Thr Ala Gln Trp Leu Leu Glu Ala Ser
            180                 185                 190

Val Ser Ser Arg Gly Glu Gln Ile Tyr Tyr Gln Tyr Arg Ala Glu Asp
        195                 200                 205

Asp Thr Gly Cys Glu Ala Asp Glu Ile Thr His His Leu Gln Ala Thr
    210                 215                 220

Ala Gln Arg Tyr Leu His Ile Val Tyr Tyr Gly Asn Arg Thr Ala Ser
225                 230                 235                 240

Glu Thr Leu Pro Gly Leu Asp Gly Ser Ala Pro Ser Gln Ala Asp Trp
                245                 250                 255

Leu Phe Tyr Leu Val Phe Asp Tyr Gly Glu Arg Ser Asn Asn Leu Lys
            260                 265                 270

Thr Pro Pro Ala Phe Ser Thr Thr Gly Ser Trp Leu Cys Arg Gln Asp
        275                 280                 285

Arg Phe Ser Arg Tyr Glu Tyr Gly Phe Glu Ile Arg Thr Arg Arg Leu
    290                 295                 300

Cys Arg Gln Val Leu Met Tyr His His Leu Gln Ala Leu Asp Ser Lys
305                 310                 315                 320
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Ile Thr Glu His Asn Gly Pro Thr Leu Val Ser Arg Leu Ile Leu Asn
                325                 330                 335

Tyr Asp Glu Ser Ala Ile Ala Ser Thr Leu Val Phe Val Arg Arg Val
            340                 345                 350

Gly His Glu Gln Asp Gly Asn Val Val Thr Leu Pro Pro Leu Glu Leu
        355                 360                 365

Ala Tyr Gln Asp Phe Ser Pro Arg His His Ala His Trp Gln Pro Met
    370                 375                 380

Asp Val Leu Ala Asn Phe Asn Ala Ile Gln Arg Trp Gln Leu Val Asp
385                 390                 395                 400

Leu Lys Gly Glu Gly Leu Pro Gly Leu Leu Tyr Gln Asp Lys Gly Ala
                405                 410                 415

Trp Trp Tyr Arg Ser Ala Gln Arg Leu Gly Glu Ile Gly Ser Asp Ala
            420                 425                 430

Val Thr Trp Glu Lys Met Gln Pro Leu Ser Val Ile Pro Ser Leu Gln
        435                 440                 445

Ser Asn Ala Ser Leu Val Asp Ile Asn Gly Asp Gly Gln Leu Asp Trp
    450                 455                 460

Val Ile Thr Gly Pro Gly Leu Arg Gly Tyr His Ser Gln Arg Pro Asp
465                 470                 475                 480

Gly Ser Trp Thr Arg Phe Thr Pro Leu Asn Ala Leu Pro Val Glu Tyr
                485                 490                 495

Thr His Pro Arg Ala Gln Leu Ala Asp Leu Met Gly Ala Gly Leu Ser
            500                 505                 510

Asp Leu Val Leu Ile Gly Pro Lys Ser Val Arg Leu Tyr Ala Asn Thr
        515                 520                 525

Arg Asp Gly Phe Ala Lys Gly Lys Asp Val Val Gln Ser Gly Asp Ile
    530                 535                 540

Thr Leu Pro Val Pro Gly Ala Asp Pro Arg Lys Leu Val Ala Phe Ser
545                 550                 555                 560

Asp Val Leu Gly Ser Gly Gln Ala His Leu Val Glu Val Ser Ala Thr
                565                 570                 575

Lys Val Thr Cys Trp Pro Asn Leu Gly Arg Gly Arg Phe Gly Gln Pro
            580                 585                 590

Ile Thr Leu Pro Gly Phe Ser Gln Pro Ala Thr Glu Phe Asn Pro Ala
        595                 600                 605

Gln Val Tyr Leu Ala Asp Leu Asp Gly Ser Gly Pro Thr Asp Leu Ile
    610                 615                 620

Tyr Val His Thr Asn Arg Leu Asp Ile Phe Leu Asn Lys Ser Gly Asn
625                 630                 635                 640

Gly Phe Ala Glu Pro Val Thr Leu Arg Phe Pro Glu Gly Leu Arg Phe
                645                 650                 655

Asp His Thr Cys Gln Leu Gln Met Ala Asp Val Gln Gly Leu Gly Val
            660                 665                 670

Ala Ser Leu Ile Leu Ser Val Pro His Met Ser Pro His His Trp Arg
        675                 680                 685

Cys Asp Leu Thr Asn Met Lys Pro Trp Leu Leu Asn Glu Met Asn Asn
    690                 695                 700

Asn Met Gly Val His His Thr Leu Arg Tyr Arg Ser Ser Ser Gln Phe
705                 710                 715                 720

Trp Leu Asp Glu Lys Ala Ala Ala Leu Thr Thr Gly Gln Thr Pro Val
                725                 730                 735
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Cys Tyr Leu Pro Phe Pro Ile His Thr Leu Trp Gln Thr Glu Thr Glu
            740                 745                 750

Asp Glu Ile Ser Gly Asn Lys Leu Val Thr Thr Leu Arg Tyr Ala Arg
        755                 760                 765

Gly Ala Trp Asp Gly Arg Glu Arg Glu Phe Arg Gly Phe Gly Tyr Val
    770                 775                 780

Glu Gln Thr Asp Ser His Gln Leu Ala Gln Gly Asn Ala Pro Glu Arg
785                 790                 795                 800

Thr Pro Pro Ala Leu Thr Lys Asn Trp Tyr Ala Thr Gly Leu Pro Val
                805                 810                 815

Ile Asp Asn Ala Leu Ser Thr Glu Tyr Trp Arg Asp Asp Gln Ala Phe
            820                 825                 830

Ala Gly Phe Ser Pro Arg Phe Thr Thr Trp Gln Asp Asn Lys Asp Val
        835                 840                 845

Pro Leu Thr Pro Glu Asp Asp Asn Ser Arg Tyr Trp Phe Asn Arg Ala
    850                 855                 860

Leu Lys Gly Gln Leu Leu Arg Ser Glu Leu Tyr Gly Leu Asp Asp Ser
865                 870                 875                 880

Thr Asn Lys His Val Pro Tyr Thr Val Thr Glu Phe Arg Ser Gln Val
                885                 890                 895

Arg Arg Leu Gln His Thr Asp Ser Arg Tyr Pro Val Leu Trp Ser Ser
            900                 905                 910

Val Val Glu Ser Arg Asn Tyr His Tyr Glu Arg Ile Ala Ser Asp Pro
        915                 920                 925

Gln Cys Ser Gln Asn Ile Thr Leu Ser Ser Asp Arg Phe Gly Gln Pro
    930                 935                 940

Leu Lys Gln Leu Ser Val Gln Tyr Pro Arg Arg Gln Gln Pro Ala Ile
945                 950                 955                 960

Asn Leu Tyr Pro Asp Thr Leu Pro Asp Lys Leu Leu Ala Asn Ser Tyr
                965                 970                 975

Asp Asp Gln Gln Arg Gln Leu Arg Leu Thr Tyr Gln Gln Ser Ser Trp
            980                 985                 990

His His Leu Thr Asn Asn Thr Val  Arg Val Leu Gly Leu  Pro Asp Ser
        995                 1000                 1005

Thr Arg  Ser Asp Ile Phe Thr  Tyr Gly Ala Glu Asn  Val Pro Ala
    1010                 1015                 1020

Gly Gly  Leu Asn Leu Glu Leu  Leu Ser Asp Lys Asn  Ser Leu Ile
    1025                 1030                 1035

Ala Asp  Asp Lys Pro Arg Glu  Tyr Leu Gly Gln Gln  Lys Thr Ala
    1040                 1045                 1050

Tyr Thr  Asp Gly Gln Asn Thr  Thr Pro Leu Gln Thr  Pro Thr Arg
    1055                 1060                 1065

Gln Ala  Leu Ile Ala Phe Thr  Glu Thr Thr Val Phe  Asn Gln Ser
    1070                 1075                 1080

Thr Leu  Ser Ala Phe Asn Gly  Ser Ile Pro Ser Asp  Lys Leu Ser
    1085                 1090                 1095

Thr Thr  Leu Glu Gln Ala Gly  Tyr Gln Gln Thr Asn  Tyr Leu Phe
    1100                 1105                 1110

Pro Arg  Thr Gly Glu Asp Lys  Val Trp Val Ala His  His Gly Tyr
    1115                 1120                 1125

Thr Asp  Tyr Gly Thr Ala Ala  Gln Phe Trp Arg Pro  Gln Lys Gln
    1130                 1135                 1140

Ser Asn  Thr Gln Leu Thr Gly  Lys Ile Thr Leu Ile  Trp Asp Ala
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    1145                1150                1155

Asn Tyr  Cys Val Val Val Gln  Thr Arg Asp Ala Ala  Gly Leu Thr
    1160                1165                1170

Thr Ser  Ala Lys Tyr Asp Trp  Arg Phe Leu Thr Pro  Val Gln Leu
    1175                1180                1185

Thr Asp  Ile Asn Asp Asn Gln  His Leu Ile Thr Leu  Asp Ala Leu
    1190                1195                1200

Gly Arg  Pro Ile Thr Leu Arg  Phe Trp Gly Thr Glu  Asn Gly Lys
    1205                1210                1215

Met Thr  Gly Tyr Ser Ser Pro  Glu Lys Ala Ser Phe  Ser Pro Pro
    1220                1225                1230

Ser Asp  Val Asn Ala Ala Ile  Glu Leu Lys Lys Pro  Leu Pro Val
    1235                1240                1245

Ala Gln  Cys Gln Val Tyr Ala  Pro Glu Ser Trp Met  Pro Val Leu
    1250                1255                1260

Ser Gln  Lys Thr Phe Asn Arg  Leu Ala Glu Gln Asp  Trp Gln Lys
    1265                1270                1275

Leu Tyr  Asn Ala Arg Ile Ile  Thr Glu Asp Gly Arg  Ile Cys Thr
    1280                1285                1290

Leu Ala  Tyr Arg Arg Trp Val  Gln Ser Gln Lys Ala  Ile Pro Gln
    1295                1300                1305

Leu Ile  Ser Leu Leu Asn Asn  Gly Pro Arg Leu Pro  Pro His Ser
    1310                1315                1320

Leu Thr  Leu Thr Thr Asp Arg  Tyr Asp His Asp Pro  Glu Gln Gln
    1325                1330                1335

Ile Arg  Gln Gln Val Val Phe  Ser Asp Gly Phe Gly  Arg Leu Leu
    1340                1345                1350

Gln Ala  Ala Ala Arg His Glu  Ala Gly Met Ala Arg  Gln Arg Asn
    1355                1360                1365

Glu Asp  Gly Ser Leu Ile Ile  Asn Val Gln His Thr  Glu Asn Arg
    1370                1375                1380

Trp Ala  Val Thr Gly Arg Thr  Glu Tyr Asp Asn Lys  Gly Gln Pro
    1385                1390                1395

Ile Arg  Thr Tyr Gln Pro Tyr  Phe Leu Asn Asp Trp  Arg Tyr Val
    1400                1405                1410

Ser Asn  Asp Ser Ala Arg Gln  Glu Lys Glu Ala Tyr  Ala Asp Thr
    1415                1420                1425

His Val  Tyr Asp Pro Ile Gly  Arg Glu Ile Lys Val  Ile Thr Ala
    1430                1435                1440

Lys Gly  Trp Phe Arg Arg Thr  Leu Phe Thr Pro Trp  Phe Thr Val
    1445                1450                1455

Asn Glu  Asp Glu Asn Asp Thr  Ala Ala Glu Val Lys  Lys Val Lys
    1460                1465                1470

Met


<210> SEQ ID NO 11
<211> LENGTH: 2883
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2880)

<400> SEQUENCE: 11

atg aaa aac att gat ccc aaa ctt tat caa aaa acc cct act gtc agc       48
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Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln Lys Thr Pro Thr Val Ser
1               5                   10                  15

gtt tac gat aac cgt ggt ctg ata atc cgt aac atc gat ttt cat cgt       96
Val Tyr Asp Asn Arg Gly Leu Ile Ile Arg Asn Ile Asp Phe His Arg
            20                  25                  30

act acc gca aat ggt gat ccc gat acc cgt att acc cgc cat caa tac      144
Thr Thr Ala Asn Gly Asp Pro Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

gat att cac gga cac cta aat caa agc atc gat ccg cgc cta tat gaa      192
Asp Ile His Gly His Leu Asn Gln Ser Ile Asp Pro Arg Leu Tyr Glu
    50                  55                  60

gcc aag caa acc aac aat acg atc aaa ccc aat ttt ctt tgg cag tat      240
Ala Lys Gln Thr Asn Asn Thr Ile Lys Pro Asn Phe Leu Trp Gln Tyr
65                  70                  75                  80

gat ttg acc ggt aat ccc cta tgt aca gag agc att gat gca ggt cgc      288
Asp Leu Thr Gly Asn Pro Leu Cys Thr Glu Ser Ile Asp Ala Gly Arg
                85                  90                  95

act gtc acc ttg aat gat att gaa ggc cgt ccg cta cta acg gtg act      336
Thr Val Thr Leu Asn Asp Ile Glu Gly Arg Pro Leu Leu Thr Val Thr
            100                 105                 110

gca aca ggg gtt ata caa act cga caa tat gaa act tct tcc ctg ccc      384
Ala Thr Gly Val Ile Gln Thr Arg Gln Tyr Glu Thr Ser Ser Leu Pro
        115                 120                 125

ggt cgt ctg tta tct gtt gcc gaa caa aca ccc gag gaa aaa aca tcc      432
Gly Arg Leu Leu Ser Val Ala Glu Gln Thr Pro Glu Glu Lys Thr Ser
    130                 135                 140

cgt atc acc gaa cgc ctg att tgg gct ggc aat acc gaa gca gag aaa      480
Arg Ile Thr Glu Arg Leu Ile Trp Ala Gly Asn Thr Glu Ala Glu Lys
145                 150                 155                 160

gac cat aac ctt gcc ggc cag tgc gtg cgt cac tat gac acg gcg gga      528
Asp His Asn Leu Ala Gly Gln Cys Val Arg His Tyr Asp Thr Ala Gly
                165                 170                 175

gtt acc cgg tta gag agt tta tca ctg acc ggt act gtt tta tct caa      576
Val Thr Arg Leu Glu Ser Leu Ser Leu Thr Gly Thr Val Leu Ser Gln
            180                 185                 190

tcc agc caa cta ttg atc gac act caa gag gca aac tgg aca ggt gat      624
Ser Ser Gln Leu Leu Ile Asp Thr Gln Glu Ala Asn Trp Thr Gly Asp
        195                 200                 205

aac gaa acc gtc tgg caa aac atg ctg gct gat gac atc tac aca acc      672
Asn Glu Thr Val Trp Gln Asn Met Leu Ala Asp Asp Ile Tyr Thr Thr
    210                 215                 220

ctg agc acc ttc gat gcc acc ggt gct tta ctg act cag acc gat gcg      720
Leu Ser Thr Phe Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala
225                 230                 235                 240

aaa ggg aac att cag aga ctg gct tat gat gtg gcc ggg cag cta aac      768
Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Val Ala Gly Gln Leu Asn
                245                 250                 255

ggg agc tgg cta aca ctc aaa ggc cag acg gaa caa gtg att atc aaa      816
Gly Ser Trp Leu Thr Leu Lys Gly Gln Thr Glu Gln Val Ile Ile Lys
            260                 265                 270

tcc ctg acc tac tcc gcc gcc gga caa aaa tta cgt gag gaa cac ggc      864
Ser Leu Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly
        275                 280                 285

aat gat gtt atc acc gaa tac agt tat gaa ccg gaa acc caa cgg ctg      912
Asn Asp Val Ile Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu
    290                 295                 300

atc ggt atc aaa acc cgc cgt ccg tca gac act aaa gtg cta caa gac      960
Ile Gly Ile Lys Thr Arg Arg Pro Ser Asp Thr Lys Val Leu Gln Asp
305                 310                 315                 320
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ctg cgc tat gaa tat gac ccg gta ggc aat gtc atc agc atc cgt aat     1008
Leu Arg Tyr Glu Tyr Asp Pro Val Gly Asn Val Ile Ser Ile Arg Asn
                325                 330                 335

gac gcg gaa gcc acc cgc ttt tgg cac aat cag aaa gtg atg ccg gaa     1056
Asp Ala Glu Ala Thr Arg Phe Trp His Asn Gln Lys Val Met Pro Glu
            340                 345                 350

aac act tat acc tac gat tcc ctg tat cag ctt atc agc gcc acc ggg     1104
Asn Thr Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly
        355                 360                 365

cgc gaa atg gcg aat ata ggt caa caa agt cac caa ttt ccc tca ccc     1152
Arg Glu Met Ala Asn Ile Gly Gln Gln Ser His Gln Phe Pro Ser Pro
    370                 375                 380

gct cta cct tct gat aac aac acc tat acc aac tat acc cgt act tat     1200
Ala Leu Pro Ser Asp Asn Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr
385                 390                 395                 400

act tat gac cgt ggc ggc aat ctg acc aaa atc cag cac agt tca ccg     1248
Thr Tyr Asp Arg Gly Gly Asn Leu Thr Lys Ile Gln His Ser Ser Pro
                405                 410                 415

gcg acg caa aac aac tac acc acc aat atc acg gtt tca aat cgc agc     1296
Ala Thr Gln Asn Asn Tyr Thr Thr Asn Ile Thr Val Ser Asn Arg Ser
            420                 425                 430

aac cgc gca gta ctc agc aca ttg acc gaa gat ccg gcg caa gta gat     1344
Asn Arg Ala Val Leu Ser Thr Leu Thr Glu Asp Pro Ala Gln Val Asp
        435                 440                 445

gct ttg ttt gat gca ggc gga cat cag aac acc ttg ata tca gga caa     1392
Ala Leu Phe Asp Ala Gly Gly His Gln Asn Thr Leu Ile Ser Gly Gln
    450                 455                 460

aac ctg aac tgg aat act cgt ggt gaa ctg caa caa gta aca ctg gtt     1440
Asn Leu Asn Trp Asn Thr Arg Gly Glu Leu Gln Gln Val Thr Leu Val
465                 470                 475                 480

aaa cgg gac aag ggc gcc aat gat gat cgg gaa tgg tat cgt tat agc     1488
Lys Arg Asp Lys Gly Ala Asn Asp Asp Arg Glu Trp Tyr Arg Tyr Ser
                485                 490                 495

ggt gac gga aga agg atg tta aaa atc aat gaa cag cag gcc agc aac     1536
Gly Asp Gly Arg Arg Met Leu Lys Ile Asn Glu Gln Gln Ala Ser Asn
            500                 505                 510

aac gct caa aca caa cgt gtg act tat ttg ccg aac tta gaa ctt cgt     1584
Asn Ala Gln Thr Gln Arg Val Thr Tyr Leu Pro Asn Leu Glu Leu Arg
        515                 520                 525

cta aca caa aac agc acg gcc aca acc gaa gat ttg caa gtt atc acc     1632
Leu Thr Gln Asn Ser Thr Ala Thr Thr Glu Asp Leu Gln Val Ile Thr
    530                 535                 540

gta ggc gaa gcg ggc cgg gca cag gta cga gta tta cat tgg gag agc     1680
Val Gly Glu Ala Gly Arg Ala Gln Val Arg Val Leu His Trp Glu Ser
545                 550                 555                 560

ggt aaa ccg gaa gat atc gac aat aat cag ttg cgt tat agt tac gat     1728
Gly Lys Pro Glu Asp Ile Asp Asn Asn Gln Leu Arg Tyr Ser Tyr Asp
                565                 570                 575

aat ctt atc ggt tcc agt caa ctt gaa tta gat agc gaa gga caa att     1776
Asn Leu Ile Gly Ser Ser Gln Leu Glu Leu Asp Ser Glu Gly Gln Ile
            580                 585                 590

atc agt gaa gaa gaa tat tat ccc tat ggt gga aca gca tta tgg gcc     1824
Ile Ser Glu Glu Glu Tyr Tyr Pro Tyr Gly Gly Thr Ala Leu Trp Ala
        595                 600                 605

gcc agg aat cag aca gaa gcc agt tat aaa act atc cgt tat tca ggc     1872
Ala Arg Asn Gln Thr Glu Ala Ser Tyr Lys Thr Ile Arg Tyr Ser Gly
    610                 615                 620

aaa gag cgg gat gcc acc ggg cta tat tac tac ggc tat cgg tat tac     1920
Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr
625                 630                 635                 640
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caa ccg tgg ata gga cgg tgg tta agc tcc gat ccg gca gga aca atc     1968
Gln Pro Trp Ile Gly Arg Trp Leu Ser Ser Asp Pro Ala Gly Thr Ile
                645                 650                 655

gat ggg ctg aat tta tat cgg atg gtg agg aat aat cca gtt acc ctc     2016
Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn Pro Val Thr Leu
            660                 665                 670

ctt gat cct gat gga tta atg cca aca att gca gaa cgc ata gca gca     2064
Leu Asp Pro Asp Gly Leu Met Pro Thr Ile Ala Glu Arg Ile Ala Ala
        675                 680                 685

cta aaa aaa aat aaa gta aca gac tca gcg cct tcg cca gca aat gcc     2112
Leu Lys Lys Asn Lys Val Thr Asp Ser Ala Pro Ser Pro Ala Asn Ala
    690                 695                 700

aca aac gta gcg ata aac atc cgc ccg cct gta gca cca aaa cct agc     2160
Thr Asn Val Ala Ile Asn Ile Arg Pro Pro Val Ala Pro Lys Pro Ser
705                 710                 715                 720

tta ccg aaa gca tca acg agt agc caa cca acc aca cac cct atc gga     2208
Leu Pro Lys Ala Ser Thr Ser Ser Gln Pro Thr Thr His Pro Ile Gly
                725                 730                 735

gct gca aac ata aaa cca acg acg tct ggg tca tct att gtt gct cca     2256
Ala Ala Asn Ile Lys Pro Thr Thr Ser Gly Ser Ser Ile Val Ala Pro
            740                 745                 750

ttg agt cca gta gga aat aaa tct act tct gaa atc tct ctg cca gaa     2304
Leu Ser Pro Val Gly Asn Lys Ser Thr Ser Glu Ile Ser Leu Pro Glu
        755                 760                 765

agc gct caa agc agt tct tca agc act acc tcg aca aat cta cag aaa     2352
Ser Ala Gln Ser Ser Ser Ser Ser Thr Thr Ser Thr Asn Leu Gln Lys
    770                 775                 780

aaa tca ttt act tta tat aga gca gat aac aga tcc ttt gaa gaa atg     2400
Lys Ser Phe Thr Leu Tyr Arg Ala Asp Asn Arg Ser Phe Glu Glu Met
785                 790                 795                 800

caa agt aaa ttc cct gaa gga ttt aaa gcc tgg act cct cta gac act     2448
Gln Ser Lys Phe Pro Glu Gly Phe Lys Ala Trp Thr Pro Leu Asp Thr
                805                 810                 815

aag atg gca agg caa ttt gct agt atc ttt att ggt cag aaa gat aca     2496
Lys Met Ala Arg Gln Phe Ala Ser Ile Phe Ile Gly Gln Lys Asp Thr
            820                 825                 830

tct aat tta cct aaa gaa aca gtc aag aac ata agc aca tgg gga gca     2544
Ser Asn Leu Pro Lys Glu Thr Val Lys Asn Ile Ser Thr Trp Gly Ala
        835                 840                 845

aag cca aaa cta aaa gat ctc tca aat tac ata aaa tat acc aag gac     2592
Lys Pro Lys Leu Lys Asp Leu Ser Asn Tyr Ile Lys Tyr Thr Lys Asp
    850                 855                 860

aaa tct aca gta tgg gtt tct act gca att aat act gaa gca ggt gga     2640
Lys Ser Thr Val Trp Val Ser Thr Ala Ile Asn Thr Glu Ala Gly Gly
865                 870                 875                 880

caa agc tca ggg gct cca ctc cat aaa att gat atg gat ctc tac gag     2688
Gln Ser Ser Gly Ala Pro Leu His Lys Ile Asp Met Asp Leu Tyr Glu
                885                 890                 895

ttt gcc att gat gga caa aaa cta aat cca cta ccg gag ggt aga act     2736
Phe Ala Ile Asp Gly Gln Lys Leu Asn Pro Leu Pro Glu Gly Arg Thr
            900                 905                 910

aaa aac atg gta cct tcc ctt tta ctc gac acc cca caa ata gag aca     2784
Lys Asn Met Val Pro Ser Leu Leu Leu Asp Thr Pro Gln Ile Glu Thr
        915                 920                 925

tca tcc atc att gca ctt aat cat gga ccg gta aat gat gca gaa att     2832
Ser Ser Ile Ile Ala Leu Asn His Gly Pro Val Asn Asp Ala Glu Ile
    930                 935                 940

tca ttt ctg aca aca att ccg ctt aaa aat gta aaa cct cat aag aga     2880
Ser Phe Leu Thr Thr Ile Pro Leu Lys Asn Val Lys Pro His Lys Arg
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945                 950                 955                 960

taa                                                                 2883


<210> SEQ ID NO 12
<211> LENGTH: 960
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 12

Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln Lys Thr Pro Thr Val Ser
1               5                   10                  15

Val Tyr Asp Asn Arg Gly Leu Ile Ile Arg Asn Ile Asp Phe His Arg
            20                  25                  30

Thr Thr Ala Asn Gly Asp Pro Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

Asp Ile His Gly His Leu Asn Gln Ser Ile Asp Pro Arg Leu Tyr Glu
    50                  55                  60

Ala Lys Gln Thr Asn Asn Thr Ile Lys Pro Asn Phe Leu Trp Gln Tyr
65                  70                  75                  80

Asp Leu Thr Gly Asn Pro Leu Cys Thr Glu Ser Ile Asp Ala Gly Arg
                85                  90                  95

Thr Val Thr Leu Asn Asp Ile Glu Gly Arg Pro Leu Leu Thr Val Thr
            100                 105                 110

Ala Thr Gly Val Ile Gln Thr Arg Gln Tyr Glu Thr Ser Ser Leu Pro
        115                 120                 125

Gly Arg Leu Leu Ser Val Ala Glu Gln Thr Pro Glu Glu Lys Thr Ser
    130                 135                 140

Arg Ile Thr Glu Arg Leu Ile Trp Ala Gly Asn Thr Glu Ala Glu Lys
145                 150                 155                 160

Asp His Asn Leu Ala Gly Gln Cys Val Arg His Tyr Asp Thr Ala Gly
                165                 170                 175

Val Thr Arg Leu Glu Ser Leu Ser Leu Thr Gly Thr Val Leu Ser Gln
            180                 185                 190

Ser Ser Gln Leu Leu Ile Asp Thr Gln Glu Ala Asn Trp Thr Gly Asp
        195                 200                 205

Asn Glu Thr Val Trp Gln Asn Met Leu Ala Asp Asp Ile Tyr Thr Thr
    210                 215                 220

Leu Ser Thr Phe Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala
225                 230                 235                 240

Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Val Ala Gly Gln Leu Asn
                245                 250                 255

Gly Ser Trp Leu Thr Leu Lys Gly Gln Thr Glu Gln Val Ile Ile Lys
            260                 265                 270

Ser Leu Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly
        275                 280                 285

Asn Asp Val Ile Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu
    290                 295                 300

Ile Gly Ile Lys Thr Arg Arg Pro Ser Asp Thr Lys Val Leu Gln Asp
305                 310                 315                 320

Leu Arg Tyr Glu Tyr Asp Pro Val Gly Asn Val Ile Ser Ile Arg Asn
                325                 330                 335

Asp Ala Glu Ala Thr Arg Phe Trp His Asn Gln Lys Val Met Pro Glu
            340                 345                 350

Asn Thr Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly
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        355                 360                 365

Arg Glu Met Ala Asn Ile Gly Gln Gln Ser His Gln Phe Pro Ser Pro
    370                 375                 380

Ala Leu Pro Ser Asp Asn Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr
385                 390                 395                 400

Thr Tyr Asp Arg Gly Gly Asn Leu Thr Lys Ile Gln His Ser Ser Pro
                405                 410                 415

Ala Thr Gln Asn Asn Tyr Thr Thr Asn Ile Thr Val Ser Asn Arg Ser
            420                 425                 430

Asn Arg Ala Val Leu Ser Thr Leu Thr Glu Asp Pro Ala Gln Val Asp
        435                 440                 445

Ala Leu Phe Asp Ala Gly Gly His Gln Asn Thr Leu Ile Ser Gly Gln
    450                 455                 460

Asn Leu Asn Trp Asn Thr Arg Gly Glu Leu Gln Gln Val Thr Leu Val
465                 470                 475                 480

Lys Arg Asp Lys Gly Ala Asn Asp Asp Arg Glu Trp Tyr Arg Tyr Ser
                485                 490                 495

Gly Asp Gly Arg Arg Met Leu Lys Ile Asn Glu Gln Gln Ala Ser Asn
            500                 505                 510

Asn Ala Gln Thr Gln Arg Val Thr Tyr Leu Pro Asn Leu Glu Leu Arg
        515                 520                 525

Leu Thr Gln Asn Ser Thr Ala Thr Thr Glu Asp Leu Gln Val Ile Thr
    530                 535                 540

Val Gly Glu Ala Gly Arg Ala Gln Val Arg Val Leu His Trp Glu Ser
545                 550                 555                 560

Gly Lys Pro Glu Asp Ile Asp Asn Asn Gln Leu Arg Tyr Ser Tyr Asp
                565                 570                 575

Asn Leu Ile Gly Ser Ser Gln Leu Glu Leu Asp Ser Glu Gly Gln Ile
            580                 585                 590

Ile Ser Glu Glu Glu Tyr Tyr Pro Tyr Gly Gly Thr Ala Leu Trp Ala
        595                 600                 605

Ala Arg Asn Gln Thr Glu Ala Ser Tyr Lys Thr Ile Arg Tyr Ser Gly
    610                 615                 620

Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr
625                 630                 635                 640

Gln Pro Trp Ile Gly Arg Trp Leu Ser Ser Asp Pro Ala Gly Thr Ile
                645                 650                 655

Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn Pro Val Thr Leu
            660                 665                 670

Leu Asp Pro Asp Gly Leu Met Pro Thr Ile Ala Glu Arg Ile Ala Ala
        675                 680                 685

Leu Lys Lys Asn Lys Val Thr Asp Ser Ala Pro Ser Pro Ala Asn Ala
    690                 695                 700

Thr Asn Val Ala Ile Asn Ile Arg Pro Pro Val Ala Pro Lys Pro Ser
705                 710                 715                 720

Leu Pro Lys Ala Ser Thr Ser Ser Gln Pro Thr Thr His Pro Ile Gly
                725                 730                 735

Ala Ala Asn Ile Lys Pro Thr Thr Ser Gly Ser Ser Ile Val Ala Pro
            740                 745                 750

Leu Ser Pro Val Gly Asn Lys Ser Thr Ser Glu Ile Ser Leu Pro Glu
        755                 760                 765

Ser Ala Gln Ser Ser Ser Ser Ser Thr Thr Ser Thr Asn Leu Gln Lys
    770                 775                 780
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Lys Ser Phe Thr Leu Tyr Arg Ala Asp Asn Arg Ser Phe Glu Glu Met
785                 790                 795                 800

Gln Ser Lys Phe Pro Glu Gly Phe Lys Ala Trp Thr Pro Leu Asp Thr
                805                 810                 815

Lys Met Ala Arg Gln Phe Ala Ser Ile Phe Ile Gly Gln Lys Asp Thr
            820                 825                 830

Ser Asn Leu Pro Lys Glu Thr Val Lys Asn Ile Ser Thr Trp Gly Ala
        835                 840                 845

Lys Pro Lys Leu Lys Asp Leu Ser Asn Tyr Ile Lys Tyr Thr Lys Asp
    850                 855                 860

Lys Ser Thr Val Trp Val Ser Thr Ala Ile Asn Thr Glu Ala Gly Gly
865                 870                 875                 880

Gln Ser Ser Gly Ala Pro Leu His Lys Ile Asp Met Asp Leu Tyr Glu
                885                 890                 895

Phe Ala Ile Asp Gly Gln Lys Leu Asn Pro Leu Pro Glu Gly Arg Thr
            900                 905                 910

Lys Asn Met Val Pro Ser Leu Leu Leu Asp Thr Pro Gln Ile Glu Thr
        915                 920                 925

Ser Ser Ile Ile Ala Leu Asn His Gly Pro Val Asn Asp Ala Glu Ile
    930                 935                 940

Ser Phe Leu Thr Thr Ile Pro Leu Lys Asn Val Lys Pro His Lys Arg
945                 950                 955                 960


<210> SEQ ID NO 13
<211> LENGTH: 2850
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2847)

<400> SEQUENCE: 13

atg aaa aac att gac cca aaa ctt tat caa cat acg ccc acc gtt aac       48
Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln His Thr Pro Thr Val Asn
1               5                   10                  15

gtc tac gat aac cgt ggc ctg acc att cgt aac atc gac ttt cac cgt       96
Val Tyr Asp Asn Arg Gly Leu Thr Ile Arg Asn Ile Asp Phe His Arg
            20                  25                  30

gac gtc gcg gga ggc gat aca gat act cgt att acc cgc cac caa tat      144
Asp Val Ala Gly Gly Asp Thr Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

gat acc cga gga cac ttg agc caa agc att gat cca cgg ctg tat gac      192
Asp Thr Arg Gly His Leu Ser Gln Ser Ile Asp Pro Arg Leu Tyr Asp
    50                  55                  60

gcc aaa caa acc aat aac tcg aca aac ccc aac ttc ctc tgg caa tac      240
Ala Lys Gln Thr Asn Asn Ser Thr Asn Pro Asn Phe Leu Trp Gln Tyr
65                  70                  75                  80

aat ctc acc ggc gac act ttg cgg aca gaa agt gtc gat gcc ggc cgt      288
Asn Leu Thr Gly Asp Thr Leu Arg Thr Glu Ser Val Asp Ala Gly Arg
                85                  90                  95

acc gta gcc ctc aat gat att gaa ggc cgt caa gtg ttg att gta acc      336
Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Gln Val Leu Ile Val Thr
            100                 105                 110

gca acc ggc gcc att cag acc cga caa tat gaa gcc aat acc ctg ccc      384
Ala Thr Gly Ala Ile Gln Thr Arg Gln Tyr Glu Ala Asn Thr Leu Pro
        115                 120                 125

ggt cgt cta tta tcc gta agt gaa caa gcc ccc gga gaa cag act ccc      432
Gly Arg Leu Leu Ser Val Ser Glu Gln Ala Pro Gly Glu Gln Thr Pro
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    130                 135                 140

cgc gtt act gag cat ttt att tgg gct ggt aat aca cag gcg gag aaa      480
Arg Val Thr Glu His Phe Ile Trp Ala Gly Asn Thr Gln Ala Glu Lys
145                 150                 155                 160

gat cat aat ctt gcc ggc cag tat gtg cgc cac tac gac aca gca gga      528
Asp His Asn Leu Ala Gly Gln Tyr Val Arg His Tyr Asp Thr Ala Gly
                165                 170                 175

gtg acg caa ctg gaa agc ctg tca ttg aca gaa aac atc tta tct caa      576
Val Thr Gln Leu Glu Ser Leu Ser Leu Thr Glu Asn Ile Leu Ser Gln
            180                 185                 190

tcc cgt cag tta tta gcc gac ggt cag gaa gca gac tgg aca ggt aac      624
Ser Arg Gln Leu Leu Ala Asp Gly Gln Glu Ala Asp Trp Thr Gly Asn
        195                 200                 205

gat gaa acc ctc tgg cag acc aaa ctc aat agc gaa act tac acg aca      672
Asp Glu Thr Leu Trp Gln Thr Lys Leu Asn Ser Glu Thr Tyr Thr Thr
    210                 215                 220

caa agc acc ttt gat gct acc ggc gct ttg ctg acc caa acc gat gca      720
Gln Ser Thr Phe Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala
225                 230                 235                 240

aaa ggc aac atg caa cgt ctg gct tac aac gtg gca gga caa tta caa      768
Lys Gly Asn Met Gln Arg Leu Ala Tyr Asn Val Ala Gly Gln Leu Gln
                245                 250                 255

ggt agc tgg ctg aca ttg aaa aac caa agt gag caa gtc att gtc aaa      816
Gly Ser Trp Leu Thr Leu Lys Asn Gln Ser Glu Gln Val Ile Val Lys
            260                 265                 270

tcc ctg acc tat tcc gcc gca ggc cag aaa ttg cgt gaa gaa cac ggt      864
Ser Leu Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly
        275                 280                 285

aat ggc gtt atc act gaa tac agc tat gaa ccg gaa act cta cga ttg      912
Asn Gly Val Ile Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Leu Arg Leu
    290                 295                 300

atc ggt acc act act cgc cgt caa tca gat agc aag gtg tta caa gat      960
Ile Gly Thr Thr Thr Arg Arg Gln Ser Asp Ser Lys Val Leu Gln Asp
305                 310                 315                 320

cta cgc tat gaa cat gat cct gta ggg aat att att agt gtc cgt aat     1008
Leu Arg Tyr Glu His Asp Pro Val Gly Asn Ile Ile Ser Val Arg Asn
                325                 330                 335

gat gca gaa gcc acc cgc ttc tgg cgc aat cag aaa ata gtc cct gaa     1056
Asp Ala Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys Ile Val Pro Glu
            340                 345                 350

aat acc tac acc tac gat tcc ctg tat cag ctt atc agt gca aca gga     1104
Asn Thr Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly
        355                 360                 365

cgt gag atg gct aac atc ggc cag caa agc aac caa ctt cct tcg cca     1152
Arg Glu Met Ala Asn Ile Gly Gln Gln Ser Asn Gln Leu Pro Ser Pro
    370                 375                 380

atc atc cct ctt cct act gat gaa aac tca tat acc aac tat act cgc     1200
Ile Ile Pro Leu Pro Thr Asp Glu Asn Ser Tyr Thr Asn Tyr Thr Arg
385                 390                 395                 400

agc tat aat tac gat cgc ggc ggc aat ttg gtt caa atc cgg cac agt     1248
Ser Tyr Asn Tyr Asp Arg Gly Gly Asn Leu Val Gln Ile Arg His Ser
                405                 410                 415

tcc ccc gcc gcc caa aat aac tac acc aca gat atc acc gtt tcg aat     1296
Ser Pro Ala Ala Gln Asn Asn Tyr Thr Thr Asp Ile Thr Val Ser Asn
            420                 425                 430

cgc agt aac cgg gca gtg ctg agt tcg cta acc tca gac cca aca cag     1344
Arg Ser Asn Arg Ala Val Leu Ser Ser Leu Thr Ser Asp Pro Thr Gln
        435                 440                 445

gtg gag gca ctg ttt gat gcc ggc gga cat caa aca aaa ttg tta ccg     1392
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Val Glu Ala Leu Phe Asp Ala Gly Gly His Gln Thr Lys Leu Leu Pro
    450                 455                 460

ggg caa gag ctg agt tgg aat aca cga ggt gaa cta aaa cag gta acg      1440
Gly Gln Glu Leu Ser Trp Asn Thr Arg Gly Glu Leu Lys Gln Val Thr
465                 470                 475                 480

cca gtc agt cgc gag agc gcc agc gat cgg gaa tgg tat cgt tac ggc      1488
Pro Val Ser Arg Glu Ser Ala Ser Asp Arg Glu Trp Tyr Arg Tyr Gly
            485                 490                 495

aac gac ggc atg cga cgg tta aaa gtc agt gag caa cag act ggc aac      1536
Asn Asp Gly Met Arg Arg Leu Lys Val Ser Glu Gln Gln Thr Gly Asn
            500                 505                 510

agc acg cag cag caa cga gta act tat ctt ccc gat ctg gag cta cgt      1584
Ser Thr Gln Gln Gln Arg Val Thr Tyr Leu Pro Asp Leu Glu Leu Arg
        515                 520                 525

aca aca caa aat ggg act act aca tca gaa gac ctg cat gct att acc      1632
Thr Thr Gln Asn Gly Thr Thr Thr Ser Glu Asp Leu His Ala Ile Thr
    530                 535                 540

gtg gga gca gca ggc cac gca caa gtg cga gtt cta cac tgg gaa act      1680
Val Gly Ala Ala Gly His Ala Gln Val Arg Val Leu His Trp Glu Thr
545                 550                 555                 560

acg cca cca gcc ggt atc aat aac aat cag ctt cgc tat agc tat gat      1728
Thr Pro Pro Ala Gly Ile Asn Asn Asn Gln Leu Arg Tyr Ser Tyr Asp
                565                 570                 575

aat ttg att ggt tcc agt caa ctt gaa ctg gat aac gca gga caa att      1776
Asn Leu Ile Gly Ser Ser Gln Leu Glu Leu Asp Asn Ala Gly Gln Ile
            580                 585                 590

atc agt cag gaa gag tat tat cca ttt ggc ggc aca gca tta tgg gca      1824
Ile Ser Gln Glu Glu Tyr Tyr Pro Phe Gly Gly Thr Ala Leu Trp Ala
        595                 600                 605

gca aga aac caa ata gaa gcc agc tac aaa atc ctc cgt tac tca ggt      1872
Ala Arg Asn Gln Ile Glu Ala Ser Tyr Lys Ile Leu Arg Tyr Ser Gly
    610                 615                 620

aaa gaa cgc gat gct acc ggg ctc tat tat tac ggc tac cgc tat tat      1920
Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr
625                 630                 635                 640

cag ccg tgg gtt ggt agg tgg tta agc gcc gat ccg gct gga aca atc      1968
Gln Pro Trp Val Gly Arg Trp Leu Ser Ala Asp Pro Ala Gly Thr Ile
                645                 650                 655

gat gga ctg aat cta tac cgg atg gtg aga aat aat ccg tca aca ctg      2016
Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn Pro Ser Thr Leu
            660                 665                 670

gtt gat att tct ggg ctt gca cct acg aaa tac aat att ccc gga ttt      2064
Val Asp Ile Ser Gly Leu Ala Pro Thr Lys Tyr Asn Ile Pro Gly Phe
        675                 680                 685

gac ttt gat gta gaa ata gat gag caa aaa aga tct aaa tta aaa cca      2112
Asp Phe Asp Val Glu Ile Asp Glu Gln Lys Arg Ser Lys Leu Lys Pro
    690                 695                 700

acg ttg ata aga atc aaa gat gaa ttt tta cat tat ggt cct gta gat      2160
Thr Leu Ile Arg Ile Lys Asp Glu Phe Leu His Tyr Gly Pro Val Asp
705                 710                 715                 720

aag ctg tta gaa gaa aaa aaa ccc ggc ctc aat gta cca gag gag cta      2208
Lys Leu Leu Glu Glu Lys Lys Pro Gly Leu Asn Val Pro Glu Glu Leu
                725                 730                 735

ttt gat aga ggt cca tcc gag aat gga gtg tca aca tta act ttc aaa      2256
Phe Asp Arg Gly Pro Ser Glu Asn Gly Val Ser Thr Leu Thr Phe Lys
            740                 745                 750

aaa gac cta ccg ata agt tgt att agc aac aca gaa tat acc ctt gat      2304
Lys Asp Leu Pro Ile Ser Cys Ile Ser Asn Thr Glu Tyr Thr Leu Asp
        755                 760                 765
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atc tta tac aac aaa cat gag act aaa cca ttc cct tac gaa aac gaa     2352
Ile Leu Tyr Asn Lys His Glu Thr Lys Pro Phe Pro Tyr Glu Asn Glu
    770                 775                 780

gca aca gtt ggc gca gat ctg gga gta ata atg tcc gtg gag ttt gga     2400
Ala Thr Val Gly Ala Asp Leu Gly Val Ile Met Ser Val Glu Phe Gly
785                 790                 795                 800

aat aaa tca ata ggt aat gcc tct gac gaa gat tta aaa gaa gaa cat     2448
Asn Lys Ser Ile Gly Asn Ala Ser Asp Glu Asp Leu Lys Glu Glu His
                805                 810                 815

ctc cca tta gga aaa tcc aca atg gat aaa aca gac ctg cca gat tta     2496
Leu Pro Leu Gly Lys Ser Thr Met Asp Lys Thr Asp Leu Pro Asp Leu
            820                 825                 830

aaa caa ggg cta atg atc gcg gag aag ata aaa agt gga aaa ggg gca     2544
Lys Gln Gly Leu Met Ile Ala Glu Lys Ile Lys Ser Gly Lys Gly Ala
        835                 840                 845

tat cct ttt cat ttt ggt gct gca ata gct gtt gta tat ggt gag gat     2592
Tyr Pro Phe His Phe Gly Ala Ala Ile Ala Val Val Tyr Gly Glu Asp
    850                 855                 860

aaa aaa gta gcc gct tca att ctg aca gat tta tct gaa cct aaa aga     2640
Lys Lys Val Ala Ala Ser Ile Leu Thr Asp Leu Ser Glu Pro Lys Arg
865                 870                 875                 880

gac gaa ggc gag tat ttg caa agt acg aga aag gta agc gca atg ttt     2688
Asp Glu Gly Glu Tyr Leu Gln Ser Thr Arg Lys Val Ser Ala Met Phe
                885                 890                 895

atc aca aac gtc aat gaa ttt cgc ggc cat gat tac cca aaa agt aaa     2736
Ile Thr Asn Val Asn Glu Phe Arg Gly His Asp Tyr Pro Lys Ser Lys
            900                 905                 910

tat agt atc gga tta gtt aca gct gaa aaa cgt cag cca gta ata agc     2784
Tyr Ser Ile Gly Leu Val Thr Ala Glu Lys Arg Gln Pro Val Ile Ser
        915                 920                 925

aaa aaa cgt gca aac ccg gaa gag gcc cct tca tca tcc aga aat aaa     2832
Lys Lys Arg Ala Asn Pro Glu Glu Ala Pro Ser Ser Ser Arg Asn Lys
    930                 935                 940

aaa ttg cat gta cat taa                                             2850
Lys Leu His Val His
945


<210> SEQ ID NO 14
<211> LENGTH: 949
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 14

Met Lys Asn Ile Asp Pro Lys Leu Tyr Gln His Thr Pro Thr Val Asn
1               5                   10                  15

Val Tyr Asp Asn Arg Gly Leu Thr Ile Arg Asn Ile Asp Phe His Arg
            20                  25                  30

Asp Val Ala Gly Gly Asp Thr Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

Asp Thr Arg Gly His Leu Ser Gln Ser Ile Asp Pro Arg Leu Tyr Asp
    50                  55                  60

Ala Lys Gln Thr Asn Asn Ser Thr Asn Pro Asn Phe Leu Trp Gln Tyr
65                  70                  75                  80

Asn Leu Thr Gly Asp Thr Leu Arg Thr Glu Ser Val Asp Ala Gly Arg
                85                  90                  95

Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Gln Val Leu Ile Val Thr
            100                 105                 110

Ala Thr Gly Ala Ile Gln Thr Arg Gln Tyr Glu Ala Asn Thr Leu Pro
        115                 120                 125
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Gly Arg Leu Leu Ser Val Ser Glu Gln Ala Pro Gly Glu Gln Thr Pro
    130                 135                 140

Arg Val Thr Glu His Phe Ile Trp Ala Gly Asn Thr Gln Ala Glu Lys
145                 150                 155                 160

Asp His Asn Leu Ala Gly Gln Tyr Val Arg His Tyr Asp Thr Ala Gly
                165                 170                 175

Val Thr Gln Leu Glu Ser Leu Ser Leu Thr Glu Asn Ile Leu Ser Gln
            180                 185                 190

Ser Arg Gln Leu Leu Ala Asp Gly Gln Glu Ala Asp Trp Thr Gly Asn
        195                 200                 205

Asp Glu Thr Leu Trp Gln Thr Lys Leu Asn Ser Glu Thr Tyr Thr Thr
    210                 215                 220

Gln Ser Thr Phe Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala
225                 230                 235                 240

Lys Gly Asn Met Gln Arg Leu Ala Tyr Asn Val Ala Gly Gln Leu Gln
                245                 250                 255

Gly Ser Trp Leu Thr Leu Lys Asn Gln Ser Glu Gln Val Ile Val Lys
            260                 265                 270

Ser Leu Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly
        275                 280                 285

Asn Gly Val Ile Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Leu Arg Leu
    290                 295                 300

Ile Gly Thr Thr Thr Arg Arg Gln Ser Asp Ser Lys Val Leu Gln Asp
305                 310                 315                 320

Leu Arg Tyr Glu His Asp Pro Val Gly Asn Ile Ile Ser Val Arg Asn
                325                 330                 335

Asp Ala Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys Ile Val Pro Glu
            340                 345                 350

Asn Thr Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly
        355                 360                 365

Arg Glu Met Ala Asn Ile Gly Gln Gln Ser Asn Gln Leu Pro Ser Pro
    370                 375                 380

Ile Ile Pro Leu Pro Thr Asp Glu Asn Ser Tyr Thr Asn Tyr Thr Arg
385                 390                 395                 400

Ser Tyr Asn Tyr Asp Arg Gly Gly Asn Leu Val Gln Ile Arg His Ser
                405                 410                 415

Ser Pro Ala Ala Gln Asn Asn Tyr Thr Thr Asp Ile Thr Val Ser Asn
            420                 425                 430

Arg Ser Asn Arg Ala Val Leu Ser Ser Leu Thr Ser Asp Pro Thr Gln
        435                 440                 445

Val Glu Ala Leu Phe Asp Ala Gly Gly His Gln Thr Lys Leu Leu Pro
    450                 455                 460

Gly Gln Glu Leu Ser Trp Asn Thr Arg Gly Glu Leu Lys Gln Val Thr
465                 470                 475                 480

Pro Val Ser Arg Glu Ser Ala Ser Asp Arg Glu Trp Tyr Arg Tyr Gly
                485                 490                 495

Asn Asp Gly Met Arg Arg Leu Lys Val Ser Glu Gln Gln Thr Gly Asn
            500                 505                 510

Ser Thr Gln Gln Gln Arg Val Thr Tyr Leu Pro Asp Leu Glu Leu Arg
        515                 520                 525

Thr Thr Gln Asn Gly Thr Thr Thr Ser Glu Asp Leu His Ala Ile Thr
    530                 535                 540
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Val Gly Ala Ala Gly His Ala Gln Val Arg Val Leu His Trp Glu Thr
545                 550                 555                 560

Thr Pro Pro Ala Gly Ile Asn Asn Asn Gln Leu Arg Tyr Ser Tyr Asp
                565                 570                 575

Asn Leu Ile Gly Ser Ser Gln Leu Glu Leu Asp Asn Ala Gly Gln Ile
            580                 585                 590

Ile Ser Gln Glu Glu Tyr Tyr Pro Phe Gly Gly Thr Ala Leu Trp Ala
        595                 600                 605

Ala Arg Asn Gln Ile Glu Ala Ser Tyr Lys Ile Leu Arg Tyr Ser Gly
    610                 615                 620

Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly Tyr Arg Tyr Tyr
625                 630                 635                 640

Gln Pro Trp Val Gly Arg Trp Leu Ser Ala Asp Pro Ala Gly Thr Ile
                645                 650                 655

Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn Pro Ser Thr Leu
            660                 665                 670

Val Asp Ile Ser Gly Leu Ala Pro Thr Lys Tyr Asn Ile Pro Gly Phe
        675                 680                 685

Asp Phe Asp Val Glu Ile Asp Glu Gln Lys Arg Ser Lys Leu Lys Pro
    690                 695                 700

Thr Leu Ile Arg Ile Lys Asp Glu Phe Leu His Tyr Gly Pro Val Asp
705                 710                 715                 720

Lys Leu Leu Glu Glu Lys Lys Pro Gly Leu Asn Val Pro Glu Glu Leu
                725                 730                 735

Phe Asp Arg Gly Pro Ser Glu Asn Gly Val Ser Thr Leu Thr Phe Lys
            740                 745                 750

Lys Asp Leu Pro Ile Ser Cys Ile Ser Asn Thr Glu Tyr Thr Leu Asp
        755                 760                 765

Ile Leu Tyr Asn Lys His Glu Thr Lys Pro Phe Pro Tyr Glu Asn Glu
    770                 775                 780

Ala Thr Val Gly Ala Asp Leu Gly Val Ile Met Ser Val Glu Phe Gly
785                 790                 795                 800

Asn Lys Ser Ile Gly Asn Ala Ser Asp Glu Asp Leu Lys Glu Glu His
                805                 810                 815

Leu Pro Leu Gly Lys Ser Thr Met Asp Lys Thr Asp Leu Pro Asp Leu
            820                 825                 830

Lys Gln Gly Leu Met Ile Ala Glu Lys Ile Lys Ser Gly Lys Gly Ala
        835                 840                 845

Tyr Pro Phe His Phe Gly Ala Ala Ile Ala Val Val Tyr Gly Glu Asp
    850                 855                 860

Lys Lys Val Ala Ala Ser Ile Leu Thr Asp Leu Ser Glu Pro Lys Arg
865                 870                 875                 880

Asp Glu Gly Glu Tyr Leu Gln Ser Thr Arg Lys Val Ser Ala Met Phe
                885                 890                 895

Ile Thr Asn Val Asn Glu Phe Arg Gly His Asp Tyr Pro Lys Ser Lys
            900                 905                 910

Tyr Ser Ile Gly Leu Val Thr Ala Glu Lys Arg Gln Pro Val Ile Ser
        915                 920                 925

Lys Lys Arg Ala Asn Pro Glu Glu Ala Pro Ser Ser Ser Arg Asn Lys
    930                 935                 940

Lys Leu His Val His
945
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<210> SEQ ID NO 15
<211> LENGTH: 2817
<212> TYPE: DNA
<213> ORGANISM: Photorhabdus luminescens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2814)

<400> SEQUENCE: 15

atg gaa aac att gac cca aaa ctt tat cac cat acg cct acc gtc agt       48
Met Glu Asn Ile Asp Pro Lys Leu Tyr His His Thr Pro Thr Val Ser
1               5                   10                  15

gtt cac gat aac cgt gga cta gct atc cgt aat att agt ttt cac cgc       96
Val His Asp Asn Arg Gly Leu Ala Ile Arg Asn Ile Ser Phe His Arg
            20                  25                  30

act acc gca gaa gca aat acc gat acc cgt att acc cgc cat caa tat      144
Thr Thr Ala Glu Ala Asn Thr Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

aat gcc ggc gga tat ttg aac caa agc att gat cct cgc ctg tat gac      192
Asn Ala Gly Gly Tyr Leu Asn Gln Ser Ile Asp Pro Arg Leu Tyr Asp
    50                  55                  60

gcc aaa cag act aac aac gct gta caa ccg aat ttt atc tgg cga cat      240
Ala Lys Gln Thr Asn Asn Ala Val Gln Pro Asn Phe Ile Trp Arg His
65                  70                  75                  80

aat ttg acc ggc aat atc ctg cga aca gag agc gtc gat gcc ggt cgg      288
Asn Leu Thr Gly Asn Ile Leu Arg Thr Glu Ser Val Asp Ala Gly Arg
                85                  90                  95

acg att acc ctc aac gat att gaa ggc cgc ccg gtg ttg acc atc aat      336
Thr Ile Thr Leu Asn Asp Ile Glu Gly Arg Pro Val Leu Thr Ile Asn
            100                 105                 110

gca gcc ggt gtc cgg caa aac cat cgc tac gaa gat aac acc ctg ccc      384
Ala Ala Gly Val Arg Gln Asn His Arg Tyr Glu Asp Asn Thr Leu Pro
        115                 120                 125

ggt cgc ctg ctc gct atc agc gaa caa gga cag gca gaa gag aaa acg      432
Gly Arg Leu Leu Ala Ile Ser Glu Gln Gly Gln Ala Glu Glu Lys Thr
    130                 135                 140

acc gag cgc ctt atc tgg gcc ggc aat acg ccg caa gaa aaa gac cac      480
Thr Glu Arg Leu Ile Trp Ala Gly Asn Thr Pro Gln Glu Lys Asp His
145                 150                 155                 160

aac ctt gcc ggt cag tgc gtc cgc cat tac gat acc gca gga ctc act      528
Asn Leu Ala Gly Gln Cys Val Arg His Tyr Asp Thr Ala Gly Leu Thr
                165                 170                 175

caa ctc aac agc ctt gcc ctg acc ggc gcc gtt cta tca caa tct caa      576
Gln Leu Asn Ser Leu Ala Leu Thr Gly Ala Val Leu Ser Gln Ser Gln
            180                 185                 190

caa ctg ctt acc gat aac cag gat gcc gac tgg aca ggt gaa gac cag      624
Gln Leu Leu Thr Asp Asn Gln Asp Ala Asp Trp Thr Gly Glu Asp Gln
        195                 200                 205

agc ctc tgg caa caa aaa ctg agt agt gat gtc tat atc acc caa agt      672
Ser Leu Trp Gln Gln Lys Leu Ser Ser Asp Val Tyr Ile Thr Gln Ser
    210                 215                 220

aac act gat gcc acc ggg gct tta ctg acc cag acc gat gcc aaa ggc      720
Asn Thr Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly
225                 230                 235                 240

aac att cag cgg ctg gcc tat gat gtg gcc ggg cag cta aaa ggg agt      768
Asn Ile Gln Arg Leu Ala Tyr Asp Val Ala Gly Gln Leu Lys Gly Ser
                245                 250                 255

tgg tta aca ctc aaa ggt cag gcg gaa cag gtg att atc aaa tcg cta      816
Trp Leu Thr Leu Lys Gly Gln Ala Glu Gln Val Ile Ile Lys Ser Leu
            260                 265                 270

acc tac tcc gcc gcc ggg caa aaa tta cgt gaa gag cac ggt aac ggg      864
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Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly Asn Gly
        275                 280                 285

att gtc act gaa tac agc tac gaa ccg gaa acc caa cgg ctt atc ggc      912
Ile Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu Ile Gly
    290                 295                 300

att acc act cgc cgt cca tca gac gcc aag gtg ttg caa gac cta cgc      960
Ile Thr Thr Arg Arg Pro Ser Asp Ala Lys Val Leu Gln Asp Leu Arg
305                 310                 315                 320

tat caa tat gac cca gta ggc aat gtc att agt atc cgt aat gat gcg     1008
Tyr Gln Tyr Asp Pro Val Gly Asn Val Ile Ser Ile Arg Asn Asp Ala
                325                 330                 335

gaa gcc act cgc ttt tgg cgc aat cag aaa gta gcc ccg gag aat agc     1056
Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys Val Ala Pro Glu Asn Ser
            340                 345                 350

tat acc tac gat tcc ctg tat cag ctt atc agc gcc acc ggg cgc gag     1104
Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu
        355                 360                 365

atg gcc aat atc ggt cag caa agc aac caa ctt ccc tct ccg gcg cta     1152
Met Ala Asn Ile Gly Gln Gln Ser Asn Gln Leu Pro Ser Pro Ala Leu
    370                 375                 380

cct tct gat aac aat acc tac acc aac tat act cgc act tat act tat     1200
Pro Ser Asp Asn Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr
385                 390                 395                 400

gac cgt ggc ggc aat ttg acg aaa att cag cat agt tca cca gcc gcg     1248
Asp Arg Gly Gly Asn Leu Thr Lys Ile Gln His Ser Ser Pro Ala Ala
                405                 410                 415

caa aat aac tac acg acg gat ata acg gtt tca aat cgc agc aac cgc     1296
Gln Asn Asn Tyr Thr Thr Asp Ile Thr Val Ser Asn Arg Ser Asn Arg
            420                 425                 430

gcg gta ctc agc aca ttg acc gca gat cca act caa gtc gat gcc tta     1344
Ala Val Leu Ser Thr Leu Thr Ala Asp Pro Thr Gln Val Asp Ala Leu
        435                 440                 445

ttt gat gcg gga ggc cat caa acc agc ttg tta tcc ggc caa gtt cta     1392
Phe Asp Ala Gly Gly His Gln Thr Ser Leu Leu Ser Gly Gln Val Leu
    450                 455                 460

act tgg aca ccg cga ggc gaa ttg aaa caa gcc aac aat agc gca gga     1440
Thr Trp Thr Pro Arg Gly Glu Leu Lys Gln Ala Asn Asn Ser Ala Gly
465                 470                 475                 480

aat gag tgg tat cgc tac gat agc aac ggc ata cgc cag cta aaa gtg     1488
Asn Glu Trp Tyr Arg Tyr Asp Ser Asn Gly Ile Arg Gln Leu Lys Val
                485                 490                 495

aat gaa caa caa act cag aat atc ccg caa caa caa agg gta act tat     1536
Asn Glu Gln Gln Thr Gln Asn Ile Pro Gln Gln Gln Arg Val Thr Tyr
            500                 505                 510

cta ccg ggg ctg gaa ata cgt aca acc cag aac aac gcc aca aca aca     1584
Leu Pro Gly Leu Glu Ile Arg Thr Thr Gln Asn Asn Ala Thr Thr Thr
        515                 520                 525

gaa gag tta cac gtt atc aca ctc ggt aaa gcc ggc cgc gcg caa gtc     1632
Glu Glu Leu His Val Ile Thr Leu Gly Lys Ala Gly Arg Ala Gln Val
    530                 535                 540

cga gta ttg cat tgg gag agc ggt aaa cca gaa gat att aat aac aat     1680
Arg Val Leu His Trp Glu Ser Gly Lys Pro Glu Asp Ile Asn Asn Asn
545                 550                 555                 560

cag ctt cgt tac agc tac gat aat ctt att ggc tcc agc caa ctt caa     1728
Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser Gln Leu Gln
                565                 570                 575

tta gat agc gac gga caa att atc agt gaa gaa gaa tat tat cca ttt     1776
Leu Asp Ser Asp Gly Gln Ile Ile Ser Glu Glu Glu Tyr Tyr Pro Phe
            580                 585                 590
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ggt ggt aca gcg ctg tgg gcg gca agg aat caa acc gaa gcc agc tat     1824
Gly Gly Thr Ala Leu Trp Ala Ala Arg Asn Gln Thr Glu Ala Ser Tyr
        595                 600                 605

aaa acc att cgt tat tct ggt aaa gag cgg gat gtt acc ggg ctg tat     1872
Lys Thr Ile Arg Tyr Ser Gly Lys Glu Arg Asp Val Thr Gly Leu Tyr
    610                 615                 620

tat tat ggc tac cgt tat tac caa ccg tgg gcg ggc aga tgg tta ggt     1920
Tyr Tyr Gly Tyr Arg Tyr Tyr Gln Pro Trp Ala Gly Arg Trp Leu Gly
625                 630                 635                 640

gca gac ccg gca gga acc att gat gga ctg aat tta tat cgc atg gtg     1968
Ala Asp Pro Ala Gly Thr Ile Asp Gly Leu Asn Leu Tyr Arg Met Val
                645                 650                 655

aga aat aac ccg gtg acg caa ttt gat gtt cag gga tta tca ccg gcc     2016
Arg Asn Asn Pro Val Thr Gln Phe Asp Val Gln Gly Leu Ser Pro Ala
            660                 665                 670

aac aga aca gaa gaa gcg ata ata aaa cag ggt tcc ttt acg gga atg     2064
Asn Arg Thr Glu Glu Ala Ile Ile Lys Gln Gly Ser Phe Thr Gly Met
        675                 680                 685

gaa gaa gct gtt tat aaa aaa atg gct aaa cct caa act ttc aaa cgc     2112
Glu Glu Ala Val Tyr Lys Lys Met Ala Lys Pro Gln Thr Phe Lys Arg
    690                 695                 700

caa aga gct atc gct gcc caa aca gag caa gaa gcc cat gaa tca ttg     2160
Gln Arg Ala Ile Ala Ala Gln Thr Glu Gln Glu Ala His Glu Ser Leu
705                 710                 715                 720

acc aac aac cct agt gta gat att agc cca att aaa aac tac acc aca     2208
Thr Asn Asn Pro Ser Val Asp Ile Ser Pro Ile Lys Asn Tyr Thr Thr
                725                 730                 735

gat agc tca caa att aat gcc gcg ata agg gaa aat cgt att acg cca     2256
Asp Ser Ser Gln Ile Asn Ala Ala Ile Arg Glu Asn Arg Ile Thr Pro
            740                 745                 750

gca gtg gaa agt tta gac gcc aca tta tct tcc cta caa gat aga caa     2304
Ala Val Glu Ser Leu Asp Ala Thr Leu Ser Ser Leu Gln Asp Arg Gln
        755                 760                 765

atg agg gta act tat cgg gtg atg acc tat gta gat aat tcc acg cca     2352
Met Arg Val Thr Tyr Arg Val Met Thr Tyr Val Asp Asn Ser Thr Pro
    770                 775                 780

tcg cct tgg cac tcg cca cag gaa gga aat agt att aat gtt ggt gat     2400
Ser Pro Trp His Ser Pro Gln Glu Gly Asn Ser Ile Asn Val Gly Asp
785                 790                 795                 800

atc gtt tcg gat aac gct tat tta tca aca tcg gcc cat cgt ggt ttt     2448
Ile Val Ser Asp Asn Ala Tyr Leu Ser Thr Ser Ala His Arg Gly Phe
                805                 810                 815

ctg aat ttt gtt cac aaa aaa gaa acc agt gaa act cga tac gtc aag     2496
Leu Asn Phe Val His Lys Lys Glu Thr Ser Glu Thr Arg Tyr Val Lys
            820                 825                 830

atg gca ttt tta acg aat gcg ggt gtc aat gtc cca gca gca tct atg     2544
Met Ala Phe Leu Thr Asn Ala Gly Val Asn Val Pro Ala Ala Ser Met
        835                 840                 845

tat aat aat gct ggc gag gag caa gta ttt aaa atg gat tta aac gat     2592
Tyr Asn Asn Ala Gly Glu Glu Gln Val Phe Lys Met Asp Leu Asn Asp
    850                 855                 860

tca aga aaa agc ctt gct gaa aaa tta aaa cta aga gtc agt gga cca     2640
Ser Arg Lys Ser Leu Ala Glu Lys Leu Lys Leu Arg Val Ser Gly Pro
865                 870                 875                 880

caa tcg gga caa gcg gaa ata tta cta cct agg gaa aca cag ttc gaa     2688
Gln Ser Gly Gln Ala Glu Ile Leu Leu Pro Arg Glu Thr Gln Phe Glu
                885                 890                 895

gtt gtt tca atg aaa cat caa ggc aga gat acc tat gta tta ttg caa     2736
Val Val Ser Met Lys His Gln Gly Arg Asp Thr Tyr Val Leu Leu Gln
            900                 905                 910
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gat att aac caa tcc gca gcc act cat aga aat gta cgt aac act tac     2784
Asp Ile Asn Gln Ser Ala Ala Thr His Arg Asn Val Arg Asn Thr Tyr
        915                 920                 925

acc ggt aat ttc aaa tca tcc agt gca aat taa                         2817
Thr Gly Asn Phe Lys Ser Ser Ser Ala Asn
    930                 935


<210> SEQ ID NO 16
<211> LENGTH: 938
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 16

Met Glu Asn Ile Asp Pro Lys Leu Tyr His His Thr Pro Thr Val Ser
1               5                   10                  15

Val His Asp Asn Arg Gly Leu Ala Ile Arg Asn Ile Ser Phe His Arg
            20                  25                  30

Thr Thr Ala Glu Ala Asn Thr Asp Thr Arg Ile Thr Arg His Gln Tyr
        35                  40                  45

Asn Ala Gly Gly Tyr Leu Asn Gln Ser Ile Asp Pro Arg Leu Tyr Asp
    50                  55                  60

Ala Lys Gln Thr Asn Asn Ala Val Gln Pro Asn Phe Ile Trp Arg His
65                  70                  75                  80

Asn Leu Thr Gly Asn Ile Leu Arg Thr Glu Ser Val Asp Ala Gly Arg
                85                  90                  95

Thr Ile Thr Leu Asn Asp Ile Glu Gly Arg Pro Val Leu Thr Ile Asn
            100                 105                 110

Ala Ala Gly Val Arg Gln Asn His Arg Tyr Glu Asp Asn Thr Leu Pro
        115                 120                 125

Gly Arg Leu Leu Ala Ile Ser Glu Gln Gly Gln Ala Glu Glu Lys Thr
    130                 135                 140

Thr Glu Arg Leu Ile Trp Ala Gly Asn Thr Pro Gln Glu Lys Asp His
145                 150                 155                 160

Asn Leu Ala Gly Gln Cys Val Arg His Tyr Asp Thr Ala Gly Leu Thr
                165                 170                 175

Gln Leu Asn Ser Leu Ala Leu Thr Gly Ala Val Leu Ser Gln Ser Gln
            180                 185                 190

Gln Leu Leu Thr Asp Asn Gln Asp Ala Asp Trp Thr Gly Glu Asp Gln
        195                 200                 205

Ser Leu Trp Gln Gln Lys Leu Ser Ser Asp Val Tyr Ile Thr Gln Ser
    210                 215                 220

Asn Thr Asp Ala Thr Gly Ala Leu Leu Thr Gln Thr Asp Ala Lys Gly
225                 230                 235                 240

Asn Ile Gln Arg Leu Ala Tyr Asp Val Ala Gly Gln Leu Lys Gly Ser
                245                 250                 255

Trp Leu Thr Leu Lys Gly Gln Ala Glu Gln Val Ile Ile Lys Ser Leu
            260                 265                 270

Thr Tyr Ser Ala Ala Gly Gln Lys Leu Arg Glu Glu His Gly Asn Gly
        275                 280                 285

Ile Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu Ile Gly
    290                 295                 300

Ile Thr Thr Arg Arg Pro Ser Asp Ala Lys Val Leu Gln Asp Leu Arg
305                 310                 315                 320

Tyr Gln Tyr Asp Pro Val Gly Asn Val Ile Ser Ile Arg Asn Asp Ala
                325                 330                 335
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Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys Val Ala Pro Glu Asn Ser
            340                 345                 350

Tyr Thr Tyr Asp Ser Leu Tyr Gln Leu Ile Ser Ala Thr Gly Arg Glu
        355                 360                 365

Met Ala Asn Ile Gly Gln Gln Ser Asn Gln Leu Pro Ser Pro Ala Leu
    370                 375                 380

Pro Ser Asp Asn Asn Thr Tyr Thr Asn Tyr Thr Arg Thr Tyr Thr Tyr
385                 390                 395                 400

Asp Arg Gly Gly Asn Leu Thr Lys Ile Gln His Ser Ser Pro Ala Ala
                405                 410                 415

Gln Asn Asn Tyr Thr Thr Asp Ile Thr Val Ser Asn Arg Ser Asn Arg
            420                 425                 430

Ala Val Leu Ser Thr Leu Thr Ala Asp Pro Thr Gln Val Asp Ala Leu
        435                 440                 445

Phe Asp Ala Gly Gly His Gln Thr Ser Leu Leu Ser Gly Gln Val Leu
    450                 455                 460

Thr Trp Thr Pro Arg Gly Glu Leu Lys Gln Ala Asn Asn Ser Ala Gly
465                 470                 475                 480

Asn Glu Trp Tyr Arg Tyr Asp Ser Asn Gly Ile Arg Gln Leu Lys Val
                485                 490                 495

Asn Glu Gln Gln Thr Gln Asn Ile Pro Gln Gln Gln Arg Val Thr Tyr
            500                 505                 510

Leu Pro Gly Leu Glu Ile Arg Thr Thr Gln Asn Asn Ala Thr Thr Thr
        515                 520                 525

Glu Glu Leu His Val Ile Thr Leu Gly Lys Ala Gly Arg Ala Gln Val
    530                 535                 540

Arg Val Leu His Trp Glu Ser Gly Lys Pro Glu Asp Ile Asn Asn Asn
545                 550                 555                 560

Gln Leu Arg Tyr Ser Tyr Asp Asn Leu Ile Gly Ser Ser Gln Leu Gln
                565                 570                 575

Leu Asp Ser Asp Gly Gln Ile Ile Ser Glu Glu Glu Tyr Tyr Pro Phe
            580                 585                 590

Gly Gly Thr Ala Leu Trp Ala Ala Arg Asn Gln Thr Glu Ala Ser Tyr
        595                 600                 605

Lys Thr Ile Arg Tyr Ser Gly Lys Glu Arg Asp Val Thr Gly Leu Tyr
    610                 615                 620

Tyr Tyr Gly Tyr Arg Tyr Tyr Gln Pro Trp Ala Gly Arg Trp Leu Gly
625                 630                 635                 640

Ala Asp Pro Ala Gly Thr Ile Asp Gly Leu Asn Leu Tyr Arg Met Val
                645                 650                 655

Arg Asn Asn Pro Val Thr Gln Phe Asp Val Gln Gly Leu Ser Pro Ala
            660                 665                 670

Asn Arg Thr Glu Glu Ala Ile Ile Lys Gln Gly Ser Phe Thr Gly Met
        675                 680                 685

Glu Glu Ala Val Tyr Lys Lys Met Ala Lys Pro Gln Thr Phe Lys Arg
    690                 695                 700

Gln Arg Ala Ile Ala Ala Gln Thr Glu Gln Glu Ala His Glu Ser Leu
705                 710                 715                 720

Thr Asn Asn Pro Ser Val Asp Ile Ser Pro Ile Lys Asn Tyr Thr Thr
                725                 730                 735

Asp Ser Ser Gln Ile Asn Ala Ala Ile Arg Glu Asn Arg Ile Thr Pro
            740                 745                 750
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Ala Val Glu Ser Leu Asp Ala Thr Leu Ser Ser Leu Gln Asp Arg Gln
        755                 760                 765

Met Arg Val Thr Tyr Arg Val Met Thr Tyr Val Asp Asn Ser Thr Pro
    770                 775                 780

Ser Pro Trp His Ser Pro Gln Glu Gly Asn Ser Ile Asn Val Gly Asp
785                 790                 795                 800

Ile Val Ser Asp Asn Ala Tyr Leu Ser Thr Ser Ala His Arg Gly Phe
                805                 810                 815

Leu Asn Phe Val His Lys Lys Glu Thr Ser Glu Thr Arg Tyr Val Lys
            820                 825                 830

Met Ala Phe Leu Thr Asn Ala Gly Val Asn Val Pro Ala Ala Ser Met
        835                 840                 845

Tyr Asn Asn Ala Gly Glu Glu Gln Val Phe Lys Met Asp Leu Asn Asp
    850                 855                 860

Ser Arg Lys Ser Leu Ala Glu Lys Leu Lys Leu Arg Val Ser Gly Pro
865                 870                 875                 880

Gln Ser Gly Gln Ala Glu Ile Leu Leu Pro Arg Glu Thr Gln Phe Glu
                885                 890                 895

Val Val Ser Met Lys His Gln Gly Arg Asp Thr Tyr Val Leu Leu Gln
            900                 905                 910

Asp Ile Asn Gln Ser Ala Ala Thr His Arg Asn Val Arg Asn Thr Tyr
        915                 920                 925

Thr Gly Asn Phe Lys Ser Ser Ser Ala Asn
    930                 935
```

We claim:

1. An isolated nucleic acid that encodes SEQ ID NO:12.

2. The isolated nucleic acid of claim **1** comprising SEQ ID NO:11.

3. A transgenic monocot cell having a genome comprising a nucleic acid sequence that encodes the protein of SEQ ID NO:12.

4. A transgenic dicot cell having a genome comprising a nucleic acid sequence that encodes the protein of SEQ ID NO:12.

5. A transgenic plant with a genome comprising a nucleic acid sequence that encodes the protein of SEQ ID NO:12.

6. The transgenic plant of claim **5**, wherein the plant is rice.

7. The transgenic plant of claim **5**, wherein the plant is maize.

8. The transgenic plant of claim **5**, wherein the plant is tobacco.

9. The transgenic plant of claim **5**, wherein the plant is cotton.

10. A seed of the transgenic plant of claim **5**, wherein the seed comprises said nucleic acid sequence.

11. A progeny of the seed of claim **10**, wherein the progeny comprises said nucleic acid sequence.

* * * * *